

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2004, 11:03:00 ; Search time 647 Seconds
(without alignments)
4033.697 Million cell updates/sec

Title: US-09-837-602-2

Perfect score: 3899

Sequence: 1 MWKLLPAGGAGGEPYRLLT.....KESSLADLPRYPYKRRR 754

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -QFWT=fastap -SUFFIX=nrnp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowsum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pet -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09837602@cgn1.1.390 @runat_06012004_104000_12487
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

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	2	393	10.1	272	9	US-09-923-876-5167	Sequence 5167, Ap
	3	393	10.1	272	12	US-09-923-876-5167	Sequence 5167, Ap
	4	312.5	8.0	315	10	US-09-960-352-8727	Sequence 8727, Ap
	5	227.5	5.8	6456	13	US-10-269-909-35	Sequence 35, Appl
	6	216	5.5	442	9	US-09-864-761-11287	Sequence 11287, A
	7	205	5.3	114	9	US-09-864-761-27987	Sequence 27987, A
	8	179.5	4.6	5373	12	US-10-369-493-25273	Sequence 25273, A
	9	179	4.6	4437	10	US-09-801-368-51	Sequence 51, Appl
	10	179	4.6	4437	12	US-10-369-493-45841	Sequence 45841, A
	11	177	4.5	5918	15	US-10-198-846-13875	Sequence 13875, A
	12	176	4.5	5641	13	US-10-032-585-6646	Sequence 6646, Ap
	13	174	4.5	5787	12	US-10-369-493-45712	Sequence 45712, A
	14	171.5	4.4	5973	13	US-10-094-466-63	Sequence 63, Appl
	15	170.5	4.4	11167	13	US-10-252-157-188	Sequence 188, App
	16	169.5	4.3	6202	15	US-10-120-988-120	Sequence 120, App
	17	169.5	4.3	9555	15	US-10-084-817-244	Sequence 244, App
	18	169.5	4.3	9678	15	US-10-198-846-10325	Sequence 10325, A
	19	167.5	4.3	7497	10	US-09-960-253-175	Sequence 175, App
	20	167.5	4.3	7792	14	US-10-044-090-359	Sequence 359, App
	21	166	4.3	8503	13	US-10-117-722-130	Sequence 130, App
	22	166	4.3	8503	15	US-10-037-270-130	Sequence 130, App
	23	165	4.2	4780	9	US-09-962-436-287	Sequence 287, App
	24	165	4.2	6316	15	US-10-198-846-11287	Sequence 11287, A
	25	164.5	4.2	4143	12	US-10-369-493-25104	Sequence 25104, A
	26	164.5	4.2	5988	10	US-09-864-864-281	Sequence 281, App
	27	164.5	4.2	5988	15	US-10-171-581-274	Sequence 274, App
	28	164.5	4.2	6115	10	US-09-292-758-131	Sequence 131, App
	29	164.5	4.2	8948	9	US-09-735-705-119	Sequence 119, App
	30	164.5	4.2	8948	10	US-09-850-176A-119	Sequence 119, App
	31	164.5	4.2	8948	11	US-09-897-778-119	Sequence 119, App
	32	164.5	4.2	8948	11	US-09-466-396A-119	Sequence 119, App
	33	164.5	4.2	8948	13	US-10-313-986-119	Sequence 119, App
	34	164.5	4.2	8948	13	US-10-117-982-119	Sequence 119, App
	35	164.5	4.2	9588	10	US-09-954-456-1848	Sequence 1848, Ap
	36	164.5	4.2	9588	13	US-10-393-892-32	Sequence 32, Appl
	37	164.5	4.2	9588	13	US-10-394-382-32	Sequence 32, Appl
	38	164.5	4.2	9588	15	US-10-146-473-1	Sequence 1, Appli
	39	164	4.2	6297	13	US-10-311-455-967	Sequence 967, App
c	40	163.5	4.2	10625	9	US-09-727-384-5	Sequence 5, Appli
	41	163.5	4.2	10625	15	US-10-023-219-3	Sequence 3, Appli
	42	163	4.2	7992	11	US-09-893-519A-140	Sequence 140, App
	43	163	4.2	8491	13	US-10-133-013-260	Sequence 260, App
	44	163	4.2	8493	14	US-10-071-766-51	Sequence 51, Appl
	45	162.5	4.2	5857	13	US-09-873-367C-305	Sequence 305, App

ALIGNMENTS

RESULT 1

US-09-917-800A-803/c
; Patent No. US20020119462A1
; Application US/09917800A
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336

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, PRIOR FILING DATE: 2001-05-22
, PRIOR APPLICATION NUMBER: US 60/295,798
, PRIOR FILING DATE: 2001-06-06
, PRIOR APPLICATION NUMBER: US 60/297,457
, PRIOR FILING DATE: 2001-06-13
, PRIOR APPLICATION NUMBER: US 60/298,884
, PRIOR FILING DATE: 2001-06-19
, PRIOR APPLICATION NUMBER: US 60/303,459
, PRIOR FILING DATE: 2001-07-09
, NUMBER OF SEQ ID NOS: 1740
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 803
, LENGTH: 475
, TYPE: DNA
, ORGANISM: Rattus norvegicus
, FEATURE:
, - OTHER INFORMATION: Genbank Accession No
US-09-917-800A-803

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Best Local Similarity:	Conservative: 10
Query Match:	Mismatches: 17
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DB:	1
Gaps:	1
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US-09-837-602-2 (1-754) x US-09-923-876-5167 (1-272)

Qy 469 AspGluGluAenGlnGluMetSerCysLysSerAlaArgIleGluThrSerCysSer 488
Db 3 GATGAAGAAATCAAGAAATCTTTCATGCAATCAGCAAGATAGAAACGCTCTGTCT 62
Qy 489 LeuLeuGluGlnThrGlnProAlaThrProSerLeuThrLysAenLysGluGlnHisLeu 508
Db 63 CTTTGTAGAACAAACACACCTGCTACACNCTCATTTGTGAAAAATAAGGACGACATCTA 122
Qy 509 SerGluAenGluProValAspThrAsnSerAspAenLeuPheThrAspThrAspLeu 528
Db 123 TCTGAGATGAGCTGTGGACACAACTCAGACAACTATTATTACAGATAGATTYA 182
Qy 529 LysSerIleValLysAenSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsn 548
Db 183 AAATCTATTGTGAAAAATCTGCCAGTAAATCTCATGTCGAGAAAAAGCTAAAAAANA 242
Qy 549 Lys 549
Db 243 AAA 245

RESULT 4

US-09-960-352-8727
; Sequence 8727, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960.352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8727
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 37-LIB34-077-Q1-E1-B10
US-09-960-352-8727

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Query Match: 8.01% Indels: 2
DB: 10 Gaps: 1

US-09-837-602-2 (1-754) x US-09-960-352-8727 (1-315)

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Qy 302 LeuArgProIleProGluAlaGluIleGlyLeuAlaValIlePheMetThrThrLysAsn 321
Db 74 CATAGAGCTATCCAGAGCAAGAAATTCGCTTAACAGTTCATTTTGTACACAGAGAG 133
Qy 322 TyrCysAspProGlnGlyHisProSerThrGlyLeuLysThrThrProGlyProSer 341
Db 134 TACTGTGATACATACGGCGGAGCCAGTACAGGATTGAAGACACAACTCCAGGTCCAAAC 193
Qy 342 LeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThrThr 361

Db 194 CTTTCCAGCCCTTAACACCCCAATGAGAGTTTAATGCCAAATGCCTCAGTGAATACACA 253
Qy 362 ThrTyrValAlaAspThrGluSerGlu-GlnAlaAspThr---TrpAspLeuSerGluAr 380
Db 254 ACATATGTAGCTGACACAGAAATCAGAAATGCGCAGATACATGATGATGATTTGACTGAAAG 313
Qy 380 g 380
Db 314 A 314

RESULT 5

US-10-269-909-35
; Sequence 35, Application US/10269909
; Publication No. US20030180747A1
; GENERAL INFORMATION:
; APPLICANT: HRUBAN, RALPH H.
; APPLICANT: ARGANI, PEDRAM
; APPLICANT: IACOBUIZIO-DONAHUE, CHRISTINE
; APPLICANT: MAITRA, ANIRBAN
; TITLE OF INVENTION: PANCREATIC CANCER DIAGNOSIS AND THERAPIES
; FILE REFERENCE: 58303(71699)
; CURRENT APPLICATION NUMBER: US/10/269,909
; CURRENT FILING DATE: 2003-10-11
; PRIOR APPLICATION NUMBER: 60/328,609
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/332,754
; PRIOR FILING DATE: 2001-11-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 6456
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-269-909-35

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Query Match: 5.83% Indels: 199
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US-09-837-602-2 (1-754) x US-10-269-909-35 (1-6456)

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Db 69 TGGTTTTTGTGTGAGCAGTGAGGCACCTCGCCACAGGCTGCCACGAGAAATGATT----- 122
Qy 22 ValGluTyrValValGlyArgLysAsnCysAlaIleLeuIleGluAenAspGlnSerIle 41
Db 123 -----TTTGTGGAGAGATGACTGTGAGCTCATGTTCAGTCT---CGTAGTGTG 170
Qy 42 SerArgAsnHisAlaValLeuThrAlaAsnPheSerValThrAsnLeuSerGlnThrAsp 61
Db 171 GATAAGCAACACGCTGTCTCACTCACTATGATGCGTCT-----ACGGAT 212
Qy 62 GluIleProValLeuThrLeuLysAspAsnSerLysTyrGlyThrPheValAsnGluGlu 81
Db 213 GAGCATTTAGTGAAGGATTG-----GGCAGCCCTCAATGGGACTTTTGTGAATGATGTA 266
Qy 82 LysMetGlnAsnGlyPheSerArgThrLeuLysSerGlyAspGlyIleThrPheGlyVal 101
Db 267 AGGATTCGGACACAGACTTATATCACCTTGAACTTCAAGATAGACTGAGATTGGATAT 326
Qy 102 PheGlySerLysPheArgIleGluTyrGluProLeuValAlaCysSerSerCysLeuAsp 121
Db 327 GATACAAATCTTTTCACTGTA----- 347
Qy 122 ValSerGlyLysThrAlaLeuAenGlnAlaIleLeuGlnLeuGlyGlyPheThrValAsn 141
Db 348 GTACAGAGGAAATGAGGGTCCCTGAGAAAGACTCTTAAGCATGAGAAAGTTTACCATTCAG 407

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Qy	142	AsnTrpThrGluGluCysThsRHisLeuValMetValSerValLysValThrIleLysThr	161
Db	408	CTTCAGTTGTCCCCAAAAATCTTCAGAAATTCAGAAATTCCTCAAAATCTGCAAGTGCCAAAAGC	467
Qy	162	IleCysAlaLeuIleCysGlyArgProIleValLysProGluTyrPheThrGluPheLeu	181
Db	468	ATAGATTCAAAGGTAGCAGACGCTGTACTGAACTGCAGCACAAAACCTACTACTGAAGCACTG	527
Qy	182	LysAlaValGlnSerLysLysGlnProProGlnIleGluSerPheTyrProProLeuAsp	201
Db	528	AAATCCGAGNAAGCCATGGATATTTCTGCTATGCCCCGTGTACTCCATATATATATGGG	587
Qy	202	GluProSer---IleGlySerLysAsnValAsp	214
Db	588	CAGCCGTATGCTGGGGGATGATGAGGTGGATGATAAAAAAGAGCTTTCAAGACAAATGGC	647
Qy	215	ArgGlnGluArgLysGlnIlePheLysGlyLysThrPheIlePheLeuAsnAlaLysGln	234
Db	648	AAACCTGAAGAAAAAACCATGAAGCTGGAAACATCAGGGTGCACATAGATGCCAAGCAA	707
Qy	235	HisLysLysLeuSerSerAlaValPheGlyGlyGlyGluAlaArgLeuIleThrGlu	254
Db	708	GTTGAGGACAACTGCGAGCT	728
Qy	255	GluAsnGluGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAspThrGly	274
Db	728	-----	728
Qy	275	IleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSerIleMet	294
Db	729	---GCAATGAAGAAGTACTTTTCTCTTCTGTAGGAA-----CCAAGTATTATTT	776
Qy	295	AspMetLeuGlnArgGlnGlyLeuArgPro-----IleProGluAlaGluIleGlyLeu	312
Db	777	GAATCCTCACAAAAGAAATTCACGACACCATCACAAATACAGAAAGCATATTTCATGAA	836
Qy	313	AlaValIlePheMetThrThrLysAsnTyrCysAspProGlnGlyHisProSerThrGly	332
Db	837	ATCCCAACAAAAGACACGCCAAGTTCCCATATACAGGTGCAGGGCATGCTTCATTTACC	896
Qy	333	LeuLys-----ThrThrThrProGlyProSerLeuSerGlnGlyValSerValAspGlu	350
Db	897	ATTGAATTTGATGACAGTACCCAGGGAAG-----GTAACATTATTAGAGAC	941
Qy	351	-----LysLeuMetProSerAlaPro-----	357
Db	942	CATGTGACAAAGTTACTTCTGTATCATCGCGCCACAAAGTCCCAAGAGTCTTCTCTGGAACT	1001
Qy	358	-----ValAsnThrThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThr	374
Db	1002	CAAGACTTGCTGGGGATTCAAACAGGAATGATGGCACCCGAAAAACAAAGTTGCTGAC---	1058
Qy	375	TrpAspLeuSerGluArgProLysGluIleLysValSerLysMetGluGlnLysPheArg	394
Db	1059	TGGCTAGCAAAACAAACCCCTCTCTCAAAATGCTATGGGAAAGAAACAGAAAGAGGATTCCTAAA	1118
Qy	395	MetLeuSerGlnAspAlaProThrValLysGluSerCysLysThrSerSerAsnAsn	414
Db	1119	AGCATTTAAAGTGAATGTTCCAGTGCTACTGAAAGGTTGAAGAAATAAACATGATGAT	1178
Qy	415	SerMetValSerAsnThr-----	421
Db	1179	GGTACGCAAAAGTGATTACAGAAAGCGCTGGGGCTCACAGGCGCTGTACGAAACGTGCAACT	1238
Qy	422	AlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIleAsnLys	441
Db	1239	CTTGAGGAACACTTTAAGACCCCAATTCAGAACACACAAAAAGCTA-----	1283
Qy	442	SerLysAspArgAlaSerGlnGlnGlnThrAsnSerIle-----	455
Db	1284	CAGAAGGTCAGGCTACTGAAAAGCATCAAGACCAAGCTGTTGTGTTGGAGTAGATGAC	1343
Qy	456	---ArgAsnTyrPheGlnProSerThrLysLysArgGluArgAspGluGluAsnGlnGlu	474

Db	1344	AAACAGGATTTATATAGGCGCTGTTATCAACGAAAAACATAAAGAT	1388
Qy	475	MetSerSerCysLysSerAlaAarglieGluThrSerCysSerLeuLeuGluGlnThrGln	494
Db	1389	-----CTAATAAAGATTGGGCTCTCAGTGTCTGCTGCAGCAGTAAATGGNAGAAAGAAA	1442
Qy	495	ProAlaThr-----	497
Db	1443	CCACTGACTACTCTGGATTTCACACTCAGAGGAAGGCACATCTTCATCTGGAAGCAA	1502
Qy	498	-----ProSerLeuTrpLysAsnLysGluClnHisLeuSerGluAsn	511
Db	1503	CGTGGGTTTCACAGTGGCGCTAGTTGGTCGCCAATCATACAGGCGATGATCAAGAAGAA	1562
Qy	512	GluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSer	530
Db	1563	AGGATAATGGAATTTCTGTCACCTCTCTCTTTAGAGAATGAGACAGAGATCAGTGAGTCT	1622
Qy	531	-----IleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsn	548
Db	1623	GGCATGACAGCTGAGAAGTAGTGGCTCTGCAACTCTCTGGCTAGCCAG---GGAGAGAGA	1679
Qy	549	LysLysArgGluMetAspValAlaIleGluAspGluValLeuGlu---GlnLeuPhe	567
Db	1680	AGGAGACGAACCTCTCCCGACGCTTCCAAATGAAGAAAAAGTCTCTTGAGGCCACAGCA	1739
Qy	568	LysAspThrLysProGluLeuGluIle-----AspValLysValGlnLysGln	583
Db	1740	AAGGTTGTTAACACAGAGGTCAGAGATAGGAGAAAAACAAGACACAGAACTTCAGGAGAAA	1799
Qy	584	GluGluAspValAsnValArgLysArgProArgMetAspIleGluThrAsnAspThrPhe	603
Db	1800	GAACACCTTACACAGGTATACCAAGAAAGATAACAAGATGCTGCAGACAGCCCTTGAGTAAA	1859
Qy	604	SerAspGluAlaVal---ProGluSerSerLysIleSerGlnGluAsnGluIleGlyLys	622
Db	1860	ATCAACAGGCGCAGTAATATGGAGAGACTCTCAAACTGGTGGAGATAAT-----	1907
Qy	623	LysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSerAsnAsnAspLys	642
Db	1908	AAAAACCTACTTCACTTAGGCAGCTCTGCTCTGGAAAAAGAGAAAAAGTGAATATAAG	1967
Qy	643	-----LeuGlnAspAsp	646
Db	1968	GAACCTCTTTGTTAAGCAACACATTAGCAAACTTCAACAACAGAACAAAGGGAGGAG	2027
Qy	647	SerGluMetLeuProLysLysLeuLeuLeuThrGluPheArgSerLeuValIleLysAsn	666
Db	2028	GCTCAGTGGACACCTTACTAAATTG-----	2051
Qy	667	SerThrSerArgAsnProSerGlyIleAsnAspAspTyrGlyClnLeuLysAsnPheLys	686
Db	2052	---TCITCCAAAATGTTTCAGGTCAGACAGATAAATGTAGGAG-----GAA	2096
Qy	687	LysPheLysLysValThrTyrProGlyAlaGlyLysLeuProHisIleIleGlyGlySer	706
Db	2097	ACTTTTAAACAGAAATCAACACCTCCAGAAAAAAATTCAGGACATCTCACAGCAAGA	2156
Qy	707	AspLeuIleAlaHisIleAlaArgLysAsnThrGluLeuGluGluTrpLeuArgGlnGlu	726
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RESULT 6

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US-09-864-761-11287
; Sequence 11287, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED

```


; APPLICANT: Hecht, Peter
 ; APPLICANT: Holtzman, Doug
 ; APPLICANT: Madden, Kevin
 ; APPLICANT: Maxon, Mary
 ; APPLICANT: Milne, Todd
 ; APPLICANT: No. US20020128250Alman, Thea
 ; APPLICANT: Royer, John
 ; APPLICANT: Salama, Sofie
 ; APPLICANT: Sherman, Amir
 ; APPLICANT: Silva, Jeff
 ; APPLICANT: Summers, Eric
 ; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
 ; FILE REFERENCE: 109272.147
 ; CURRENT APPLICATION NUMBER: US/09/801,368
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 09/487,558
 ; PRIOR FILING DATE: 2000-01-19
 ; PRIOR APPLICATION NUMBER: US 60/160,587
 ; PRIOR FILING DATE: 1999-10-20
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 51
 ; LENGTH: 4437
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-09-801-368-51

Alignment Scores:
 Pred. No.: 3.36e-07 Length: 4437
 Score: 179.00 Matches: 108
 Percent Similarity: 38.92% Conservative: 87
 Best Local Similarity: 21.56% Mismatches: 167
 Query Match: 4.59% Indels: 139
 DB: 10 Gaps: 21

US-09-837-602-2 (1-754) x US-09-801-368-51 (1-4437)

QY 324 AspProGlnGlyHisProSerThrThrGlyLeuLysThrThrThrProGlyProSerLeuSer 343
 DB 1156 AATCCCAAGGTCTAT-----AGTCTGTCTAGTGAATTTAGCT 1194
 QY 344 GlnGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThrThrThrThr 363
 DB 1195 AAAGGAAATCTTAACACTATGAACTAATGTCTTCACTTTAAACAACTTCTCA 1251
 QY 364 ValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArgProLysGlu 383
 DB 1252 ---CTACCCACTTCGGATGATAAAGGTAAATTATGGATTAATTCAAAGAAAGAGCCAA 1308
 QY 384 IleLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAlaProThrVal 403
 DB 1309 ATAGGGGTTCTAGCCCAATACGGTAGCTTATGTAACGTTCTCAAGAAACTCCATCCTTA 1368
 QY 404 LysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeuAlaLys 423
 DB 1369 AAA-----TCGAATTCGAGTACTGTACTTAAACCGTACAAACGGCAGAT 1413
 QY 424 MetArgIleProAsnThrGlnLeuSerProThrLysLeuProSerIleAsnLysSerLys 443
 DB 1414 GTAATATACATCTCCATCTTCATCACA-----CGCCAAATACCCAAACTGCA 1464
 QY 444 AspArgAlaSerGlnGlnGlnGlnThrAsnSerIleArgAsnThrPheGlnProSerThr 463
 DB 1465 AACAGAAGTTTGGAGGTTCATCAGCACA----- 1491
 QY 464 LysLysArgGluArgAspGluGluAsnGlnGluMetSerSerCysLysSerAlaArgIle 483
 DB 1492 -----GAAGATACACCTAAAAATTTCTTCAACACCGGCTCTTTTAA 1533
 QY 484 GluThr-----SerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrp 501
 DB 1534 GAACCGTATCTGATTGTATTAATCCAGACAAGACAGTTCAGTCCGGTAAATAATCA 1593

RESULT 10

US-10-369-493-45841
 ; Sequence 45841, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:

QY 502 LysAsnLysGluGlnHisLeu----- 508
 DB 1594 AAGTATAGTGTAAAGAACTTTTATCTGGACCAAAATTTTATCTCTGAAGAAACAGGG 1653
 QY 509 -----SerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp 525
 DB 1654 TTAATGATAGTAGAATAAATATATCTCGTTACCAAGATATGTTAGTTTGTTCGG 1713
 QY 526 ThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeu 545
 DB 1714 CTAAACTTAAAGAGTAGCAAAATATCCAGITTCAAAGAACTCTCTCACAATAATG 1773
 QY 546 ArgSerAsnLysLysArg-----GluMetAspAsp-----Val 556
 DB 1774 GGAATCAATCACAAAAATGTCACTTTCCATATGACAGACTTTGATTCGGATATTGGTGT 1833
 QY 557 AlaIleGluAspGluValLeuGlu-----GlnLeuPheLysAspThrLysPro 572
 DB 1834 GCAATTCAGATGATCTTTGGAAATTTTGAAGAAAGCTGTGTTTGAACACTTCTGGA 1893
 QY 573 GluLeuGluIle-----AspValLysValGlnLysGln----- 583
 DB 1894 AAAATTTATATCAAGACCAAAATGAAGCTTCAACAAACCGAACCTGTCTCTCACC 1953
 QY 584 ---GluGluAspVal-----AsnValArgLysArgProArgMetAspIleGluThr 599
 DB 1954 TCAGAAACCAATGTCTTTTAAATCGGTGAAAGTAAAGAGTTCAATGAGGTCCGGAACA 2013
 QY 600 AsnAspThrPheSerAsp-----GluAlaValProGluSerSerLysIleSer 615
 DB 2014 AGCAGTCTGATAGCATCGACAGATGATGTTTCCATTTGCTCTCTCTGACATAACA 2073
 QY 616 GlnGluAsnGlu----- 619
 DB 2074 TCATTTGATGAACATGCATCAGGAAGTGGCGGAGGTACCCCAACCCCGAGTTATTAC 2133
 QY 620 -----IleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGlu 636
 DB 2134 TATGACAGAGTTTCCAATACTAATCCAACCTGAAGATTGAATTTATTTGGAATATTAAAGAA 2193
 QY 637 IleSerAsnAsnAspLysLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLeu 656
 DB 2194 GTTCTTCTCATGAG-----GAAATATGCACCAAAATGGTTTAAAA 2235
 QY 657 ThrGluPheArg-----SerLeuValIleLysAsnSerThrSerArgAsnProSer 673
 DB 2236 ACAAGTCCAAATTAGAATCAACCTACAGATTAAGGAAGTAAATTAATATTCTTACC 2295
 QY 674 GlyIleAsnAspAspThrGlyGlnLeuLysAsnPheLysLysPheLysValThrTrp 693
 DB 2296 CCCTAAACAGAAATGAAGCAAG---AGTAGTTTCAAGTGTCTAAGAAAA----- 2343
 QY 694 ProGlyAlaGlyLysLeuProHisIleIleGlyLysSerAspLeuIleAlaHisAla 713
 DB 2343 ----- 2343
 QY 714 ArgLysAsnThrGluLeuGluTrpLeuArgGlnGluMetGlu-ValGlnAsnGln-- 732
 DB 2344 GATGAGGGAGCTGAATTTGATTTCAATCATCTGATGGAATCGCTTATACAAACCAAGAA 2403
 QY 733 ----HisAlaLysGluGlu-----SerLeuAlaAspAspLeuPheArgTrpAsnProTy 749
 DB 2404 CTGGCACCACCAAGAGAGAGCTCCCAAGCTCCCGCAAAATACTTCTCTCAGAGACCTTA 2463
 QY 749 r 749
 DB 2464 T 2464

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 45841
LENGTH: 4437
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-10-369-493-45841

Alignment Scores:
Pred. No.: 3.36e-07 Length: 4437
Score: 179.00 Matches: 108
Percent Similarity: 38.92% Conservatives: 87
Best Local Similarity: 21.56% Mismatches: 167
Query Match: 4.59% Indels: 139
DB: 12 Gaps: 21

US-09-837-602-2 (1-754) x US-10-369-493-45841 (1-4437)

QY 324 AsproGlnGlyHisProSerThrGlyLeuLysThrThrProGlyProSerLeuSer 343
DB 1156 AATCCCAAGGTCTAT-----AGTCTGTCTAGTGAATTTAGCT 1194

QY 344 GlnGlyValSerValAspGluLysLeuMetProSerAlaProValAenThrThrTyr 363
DB 1195 AAGGAAATCTAACTAATAAGTAAATTTATGGAATAAATTCACCAATCTTCA 1251

QY 364 ValAlaAspThrGluSerGluGlnAlaAspThrTyrAspLeuSerGluArgProLysGlu 383
DB 1252 ---CTACCCACTTCGGATGATAAGGTAATTTATGGAATAAATTCACCAAGAGCCAA 1308

QY 384 IleLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAlaProThrVal 403
DB 1309 ATAGGGTCTCTACCCCAATACGGTAGCTTATGTAACGCTCTCAAGAACTCCATCCTTA 1368

QY 404 LysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeuAlaLys 423
DB 1369 AAA-----TGAATTCGAGTACTGCTACCTTAACCGTACAAACGGCAGAT 1413

QY 424 MetArgIleProAsnThrGlnLeuSerProThrLysLeuProSerIleAsnLysSerLys 443
DB 1414 GTAATATACCATCTCCATCTCTCATCACC-----CGCCCAATACCCAAACTGCA 1464

QY 444 AspArgAlaSerGlnGlnGlnThrAsnSerIleArgAsnThrPheGlnProSerThr 463
DB 1465 AACAGAGTTTGGAGGTATCATCAGCACA-----1491

QY 464 LysLysArgGluArgAspGluGlnAsnGlnGluMetSerSerCysLysSerAlaArgIle 483
DB 1492 -----GAAGATACACCTTAATTTCTTCAACCGCGCTCTTTTAA 1533

QY 484 GluThr-----SerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrp 501
DB 1534 GAAACGTATCTGATTTGATTAATCCAGACAGACAGTTCAGTCGCGGTAAATATCA 1593

QY 502 LysAsnLysGluGlnHisLeu-----508
DB 1594 AAGTATAGTGAAGAACTTTTACTCGACCAAAATTTTATCTCTGAAGAAACAGGG 1653

QY 509 -----SerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp 525
DB 1654 TTAATCATAGTGAATAATATATTCTGGTACCAGAAAGTATGTAGTTTGTTCGG 1713

QY 526 ThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaGluLysLeu 545
DB 1714 CTAACCTTAAAGAGTGTAGCAAAATATCCAGTTTCAAGAAATCTCTCACAATAATG 1773

QY 546 ArgSerAsnLysLysArg-----GluMetAspAsp-----Val 556
DB 1774 GGAATCAATCACAAAAATGTCACTTTCCATATGACAGACTTTTGATTGCGATATTGGTGT 1833

QY 557 AlaIleGluAspGluValLeuGlu-----GlnLeuPheLysAspThrLysPro 572
DB 1834 GCAATTCAGATGATACTTTGGAAATTTTGAATAAAGAGCTTTGTTTGAACACTTCTGGA 1893

QY 573 GluLeuGluIle-----AspValLysValGlnLysGln-----583
DB 1894 AAAATTTATATCAAGACCAAAATGAAGCTTCAACAAACCCGAAACCTGCTCTCTCACC 1953

QY 584 ---GluGluAspVal-----AsnValArgLysArgProArgMetAspIleGluThr 599
DB 1954 TCAGAAACCAATGTCTCTTTAAATCGTGAAAGTAAGAGTTTCAATGAGGTCCGGAACA 2013

QY 600 AsnAspThrPheSerAsp-----GluAlaValProGluSerSerLysIleSer 615
DB 2014 AGCAGTCTGATGATCGACAGATGATTTTCCATTTGTCACCTCGTCTTCTGACATAACA 2073

QY 616 GlnGluAsnGlu-----619
DB 2074 TCATTTTGATGAACATCATCAGGAAGTGGCGCAGGTACCCCAACCCGAGTTATTAC 2133

QY 620 -----IleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGlu 636
DB 2134 TATGACAGAGTTTCCAAATACTAATCAACTGAGAAATTTGAATATTGAATATTAAAGAA 2193

QY 637 IleSerAsnAsnAspLysLeuGlnAspSerGluMetLeuProLysLysLysLeuLeu 656
DB 2194 GTTCTTTCATGAG-----GAAATGCACCAAAATGGTTTTTAA 2235

QY 657 ThrGluPheArg-----SerLeuValIleLysAsnSerThrSerArgAsnProSer 673
DB 2236 ACAAGTCCAAATTAGAATCTCAACCTACAGATAAAGGAAGTAAATTAATATTCTCTACC 2295

QY 674 GlyIleAsnAspAspTyrGlyGlnLeuLysAsnPheLysLysLysValThrTyr 693
DB 2296 CCATTAACAGAAATGAAGCAAG---AGTAGTTTTCAAGTCTGAAGAAA-----2343

QY 694 ProGlyAlaGlyLysLeuProHisIleGlySerAspLeuIleAlaHisAla 713
DB 2343 -----2343

QY 714 ArgLysAsnThrGluLeuGluTrpLeuArgGlnGluMetGlu-ValGlnAsnGln-- 732
DB 2344 GATGAGGGACTGAAATTTGATTTCAATCATCGTAGGGAATCGGCTTATACAAACCCAGAA 2403

QY 733 ----HisAlaLysGluGlu-----SerLeuAlaAspAspLeuPheArgTyrAsnProTy 749
DB 2404 CTGGCACCACCAAGAGAGAGCTCCCAAGCTCCCGCAATATCTTCTCTCAGAGACCTTA 2463

QY 749 r 749
DB 2464 T 2464

RESULT 11

US-10-198-846-13875
Sequence 13875, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049

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; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13875
; LENGTH: 5918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13875

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Alignment Scores:	
Pred. No.:	8.23e-07
Score:	177.00
Percent Similarity:	34.39%
Best Local Similarity:	20.96%
Query Match:	4.54%
DB:	15
Alignments:	15
Gaps:	41
Indels:	313
Mismatches:	267
Conservative:	125
Matches:	187
Length:	5918

US-09-837-602-2 (1-754) x US-10-198-846-13875 (1-5918)

Qy	17	ArgLeuLeuThrGlyValGluTyrValValGlyArgLysAsnCysAlaIleLeuLeuGlu	36
Db	1242	CGGGTGAAGGTGGGTACGAGTATGTACCAAGGGCGAGAGTGTACAGCAGGTGTACTAT	1301
Qy	37	AsnAspGlnSerIleSerArgAsnHisAlaValLeuThrAlaAsnPheSerValThrAsn	56
Db	1302	TCCATCGGGGCATGGCCCAAGTCAGTGATACGAGAAGATGTTCAACTGGATGGTGACACGC	1361
Qy	57	LeuSerGlnThrAspGlu-----	68
Db	1362	ATCAACGACACCTGGAGACCAAGCAGCCAGCCAGTCATTTCATAGTGTCTCTGGACATC	1421
Qy	69	LysAsp-----AsnSerLysTyrGlyThrPheValAsn-----Glu	80
Db	1422	GCCGGCTTTGAGATCTTTGATTTTCAACAGCTTTGAGCAGCTGTGCATCAACTTCACCAAT	1481
Qy	81	GluLysMetGlnAsnGlyPheSerArgThrLeu-----	91
Db	1482	GAGAAGCTGCAGCAGTTCCTTCAACACCACCATGTTCTGCTGGAGCAGGAGGTACAAAG	1541
Qy	92	LysSerGlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrGlu	111
Db	1542	AAGGAGGCATCGAGTGCAGTTTATTGACTTCGGCATGCACCTGCAG-----	1589
Qy	112	ProLeuValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAla	131
Db	1590	-----GCCTGCATCGACTCTCATCGAAGGCCATCGGGCATCATGTCC	1631
Qy	132	IleLeuGlnLeuGlyGlyPheThrValAsnAsnTrpThrGluGluCysThrHisLeuVal	151
Db	1632	ATCCTGGAG-----GAGGAGTGC-----	1649
Qy	152	MetValSerValLysValThrIleLysThrIleCysAlaLeuIleCysGlyArgProIle	171
Db	1650	----ATGTTCCCCAAGGCCACGGACATGACCTTCAAGGCCAAGCTGTACGACCAACCACCTG	1706
Qy	172	ValLysProGluTyrPheThrGluPheLeuLysAlaValGlnSerLysLysGlnPro---	190
Db	1707	GGCAAGTCCAACTTCCAGNAG---CCTCGCAATGTCAAGGGGAAGCAGGACCCAC	1763
Qy	191	-----ProGlnIleGluSer	195
Db	1764	TTCTCTCTGTCCACTATGTGGCACCCTGGACTCAACATCTTTGGCTCGCTGGAGAAAG	1823
Qy	196	PheTyrProProLeuAspGluProSerIleGly-----SerLysAsnValAspLeu	212
Db	1824	AACNAGACCTCTCAACGAGACGGTGGTGGCTGTACCAAGAGTCTCTCCTCAAACTC	1883
Qy	213	-----SerGlyArg	215
Db	1884	ATGSCCACACTTCTCCACCTATGCTTCTGCTGATCCGGTGTACGTGGGAAGGCAGA	1943

Qy	216	GlnGluArgLysGlnIlePheLysGlyLeuThrPheIlePheLeuAenAlaLysGlnHis	235
Db	1944	GGAGGCAAGAAG-----AAAGGCTCATCTTCCAGACAGTGTCTCTCTCCACCGG	1994
Qy	236	LysLysLeuSerSerAlaValPheGlyGlyGlyGluAlaArgLeuIleThrGluGlu	255
Db	1995	GAAAATCTGAAC-----AAGCTGATGACAAACCTG	2024
Qy	256	AsnGluGluGluHisAsnPhePhe-----LeuAlaProGly	267
Db	2025	AGGACCACCACCTCCTCACTTGTGCGCTGCATCATCCCAATGAGCGGAGGCTCCAGGG	2084
Qy	268	ThrCysValValAspThrGlyIleThrAsnSerGlnThrLeu-----	281
Db	2085	-----GTGATGACAAACCCCTGGTCATGCACACGAGTCGCATGCAACGAGTGCTGGAG	2138
Qy	282	---IleProAspCysGlnLysLysTrpIleGlnSerIleMet-----AspMetLeuGln	298
Db	2139	GGTATCGCATCTGTAGGAAGGGCTTCCCAACCGCATCTTTATGGGACTTCCGGCAG	2198
Qy	299	Arg---GlnGlyLeuArgPro-----IleProGlu-----	307
Db	2199	AGGTATCGAATCTGAACCCGACGAGCCATCCCTGAGGGCAATTCATTGATAGCAGAAA	2258
Qy	308	---AlaGluIleGlyLeuAlaValIle-PheMetThrThrLysAsn-----	321
Db	2259	GGGGCTGAGAAGCTGTCTGGGCTCCCTGGACATTGACCACACCATGAAGTTTGGCCAC	2318
Qy	322	-----TyrCysAspProGlnGlnI	327
Db	2319	ACCAAGGTGTTTCAAGGGGGGCTGCTGGGGCTGCTGGAGGAGATGCGAGATGAGAGG	2378
Qy	327	Y-----HisProSerThrGlyLeuLys-----	334
Db	2379	CTGAGCGGCATCATCACAGATCCAGGCTCAAGGCTCAAGCCGAGCCAGCTCATCGCGATTGAG	2438
Qy	335	-----ThrThrThrProGlyPr	340
Db	2439	TTCAAGAAGATGTTGGAGCGCAGGGAGCCCTGCTGGTATTCCAGTGGAAACATCCGGCC	2498
Qy	340	oSerLeu-SerGlnGlyValSerValAspGlnLysLeuMetProSer-AlaProValAsn	359
Db	2499	TTCATGGGGTCAAGAATTGGCGCTGGATGAAGCTCTACTTCAAGATCAAGCCGCTGCTG	2558
Qy	360	ThrThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGlu	379
Db	2559	AAAGGC-----GCAGAGACAGAGAGGAGATGGCCAACTGAAGAAGAGGATTCGGG	2609
Qy	380	ArgProLys-----GluIleLysValSerLysMetGluGlnLysPhe	393
Db	2610	CGAGTCAAGATGCATAGAGAAGTCTGAGGCTCGCCCAAGGAGCTGGAGGAGAGATG	2669
Qy	394	ArgMetLeuSerGlnAspAlaProThrValLysGluSerCysLysThrSerSerAsnAsn	413
Db	2670	GTGTCCCTGCTGCAGGAGAGAAGATGACCTGCAGCTCCCAAGTGCAGCGGGAACAAGACAAC	2729
Qy	414	AsnSerMetValSerAsnThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerPro	433
Db	2729	-----	2729
Qy	434	ThrLysLeuProSerIleAsnLysSerLysAspArgAlaSerGlnGlnGlnThrAsn	453
Db	2730	-----CTGGCAGATGCCGAGGAGCGCTGCCACCA-----	2755
Qy	454	SerIleArgAsnTyrPheGlnProSerThrLysLysArg-----GluArgAspGlu	470
Db	2760	CTGATCAAGAACAAGATCCAGCTGGAGGCCCAAGGTGAAGGAGATGACCGAGAGCTGGAG	2819
Qy	471	GluAsnGlnGluMetSer-----SerCysLysSerAlaArgIleGluThrSerCys	487
Db	2820	GACGAGGAGGAGATGAACGCGCGAGCTCACGGCCAAAGAGCGCAAGCTGGAAGACGATGC	2879

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Qy 488 Ser---LeuLeuGluGlnThrGlnProAlaThrProSerLeuTrpLys---AsnLysGlu 505
Db 2880 TCAGAGCTCAAGAAAGATATCGATGACCTGAGCTGACCTGCGCAAGGTGGAGAGGAA 2939

Qy 506 GlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp 525
Db 2940 AAGCAGCAACAGAGAAACAAG----- 2960

Qy 526 ThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeu 545
Db 2961 -----GTTAAACCTTGACAGAGAGATGCGCGGTGACAGGATCATGTGCAAGCTG 3014

Qy 546 ArgSerAsnLysLys-----ArgGluMetAspAspValAlaIle 558
Db 3015 ACCAAGGAGAGAAAGCTCTTCAAGAGCGCCACCAGCAAGCCCTAGATGACCTTCAGGCT 3074

Qy 559 GluAspGluValLeuGluGlnLeuPheLysAspThrLysProGluLeuGluIleAspVal 578
Db 3075 GAGGAAGACAAAGGTCAACACACTG-----ACCAAGTCTAAAGTCAAGCTGGAGCAG 3125

Qy 579 LysValGlnLysGlnGluAspValAsnValArgLysArgProArgMetAspIleGlu 598
Db 3126 CAGGTGATGATCTGAGGAGATCCCTGAGCAGAGAGAGGTGCGCATGGACCTGGAG 3185

Qy 599 ThrAsnAspThrPheSerAspGluAlaValProGluSerSerLysIleSerGlnGluAsn 618
Db 3186 CGA----- 3188

Qy 619 GluIleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSer 638
Db 3189 -----GCAAGCGGAGCTGGAGGTGACCTGAAGCTGACCCAGGAGGATCATG 3239

Qy 639 Asn-----AsnAspLysLeuGlnAspSerGluMetLeuProLysLysLeuLeuLeu 656
Db 3240 GACTGAGAACGACCAAGCTTCAG-----CTGGAGAAAGCTCAAGAG 3284

Qy 657 ThrGluPheArgSerLeuValIleLysAsnSerThrSerArgAsnProSerGlyIleAsn 676
Db 3285 AAAGAGTTT-----GACATCAGTCAGCAGAGACAGTAAATAGAG 3323

Qy 677 AspAspTyrGly-----GlnLeuLysAsnPheLysLysPheLysValThrTyrProGly 695
Db 3324 GATGAGCAGGCGCTGGCGCTTCAGCTGCAGAGAACTGAAGGAA----- 3368

Qy 696 AlaGlyLysLeuProHisIleIleGlySerAspLeuIleAlaHisHisAlaArgLys 715
Db 3369 -----AACCGGCGCAGC 3380

Qy 716 AsnThrGluLeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLys 735
Db 3381 ATCCAGGAGCTGGAGGAGGAGCTAGAGCGGAG-----GCGACAGCGCGGCGCAAG 3431

Qy 736 GluGluSerLeuAlaAspAspLeuPheArg 745
Db 3432 GTGGAGAGGCTGCGCTCAGACCTGACCCGG 3461

RESULT 12
US-09-837-602-2
; Sequence 6646, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032.585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6646
; LENGTH: 5641
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; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-6646

Alignment Scores:
Pred. No.: 9,65e-07 Length: 5641
Score: 176.00 Matches: 96
Percent Similarity: 41.50% Conservative: 87
Best Local Similarity: 21.77% Mismatches: 168
Query Match: 4.51% Indels: 90
DB: 13 Gaps: 21

US-09-837-602-2 (1-754) x US-10-032-585-6646 (1-5641)
Qy 367 ThrGluSerGluGlnAlaAspThrTrpAsp-----LeuSerGluArgProLysGluIle 384
Db 2236 ACCGAAAGGAAATCCGGAAGCAATGATAAGAAATGGAATGAAAGATTGAGAACTA 2295

Qy 385 Lys-----ValSerLysMetGluGlnLysPheArgMetLeuSerGlnAspAlaProThr 402
Db 2296 ACTAATCTTTCCACCAAACTCGAAACAAAGCTCGAAGACAAAGAAATGGCCAAA 2355

Qy 403 ValLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeuAla 422
Db 2356 ATCCAGAAGATCACAACTGCTTAATGAAAGTTCTTGTCTACGCCAACAGTTTATGC 2415

Qy 423 LysMetArgIle-----ProAsnTyrGln----- 430
Db 2416 GGCATAAAGCTCGGACGAAAGAGAGCGGAACTATTTCAGGCGCGATCAACAAGACTA 2475

Qy 431 -----LeuSerProThrLysLeuProSerIleAsnLysSer 442
Db 2476 CAAGAGGCTTTGAAAAAGGTAACACTTCTGAAAGCACATTGAAGCAATTGAAAGAAAA 2535

Qy 443 LysAspArgAlaSerGlnGlnGln-----ThrAsnSerIleArg 456
Db 2536 CTTGATTCACAGACAGACGACGCAAAAGAAATTAGAAGATGGTATCAATAATATGACTAGA 2595

Qy 457 AsnTyrPhe-----GlnProSerThrLysLysArgGlu 467
Db 2596 GACTTATTCATCTTAAAAAACTGAAGAGTGAAGCTGAAACTCAAATCAACAACGTTGAA 2655

Qy 468 ArgAspGluGluAsn-----GlnGluMetSerSerCysLysSerAlaArgIleGluThr 485
Db 2656 AGAGAGTTTAAAAAATTTGACTTATGAATTTGAAACACATAAAAG--GATTATGAATTA 2712

Qy 486 SerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGlu 505
Db 2713 CAAATTAATTAATTTGAATAAAATCAAAAT-----AATGAATTCAAACAGAAATA 2760

Qy 506 GlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp 525
Db 2761 AATGAATTTGAGTAAGAAA-----ATCGAATCTTTGACTGAAGATAATAATTAATGCC 2814

Qy 526 ThrAspLeuLysSerIleValLysAsnSer---AlaSerLysSerHisAlaAlaGluLys 544
Db 2815 AAGCAACTTGAAGAGAGTTTAAGAGATACAGAGAAACAAATGAACATTTGATGGATAAA 2874

Qy 545 LeuArgSerAsnLysLysArgGluMetAspValAlaIleGluAspGluValLeuGlu 564
Db 2875 TTGAGATCTCATCAGTTGATGATCAATGCTTGAAGGCGGAAATCAGAAATCTTGAGAA 2934

Qy 565 GlnLeuPheLysAspThrLysProGluLeuGlu---IleAspValLysValGlnLysGln 583
Db 2935 GAAACAGTTAAA--GCCAAGAGAGAGTTGGAACACCTTACCAGTAGATGATAATCTT 2991

Qy 584 GluGluAspValAsnValArgLysArgProArgMetAspIleGlu----- 598
Db 2992 GAAAGGAATTGAAGGAACAACAATCTAAAAAAATGAATTTGGAAGGACAGCTTACAAAAT 3051

Qy 599 -----ThrAsnAspThrPheSerAsp-----GluAlaValPro 609
Db 3052 ATTACTGATTTCTACCAATGAAAGTTTAAAGAAATTAGAGAGTGAATTTGAAGGATATCAA 3111
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Qy	326	GlnGlyHisProSerThrGlyLeu-----LysThrThrThrProGlyPro	340
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Qy	341	SerLeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThr	360
Db	1623	GCCCGCATAAAGACGTGGAGAGGAACAAGCCCTCCACCNAGCGGTGACGGAGGCC	1682
Qy	361	ThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArg	380
Db	1683	AATGGCAAGCTCAGCCAGTTGGAGTTTGAGAAAGCGGCAGCTGCACGGACTTGGAGCAG	1742
Qy	381	ProLysGlu-----IleLysValSerLysMetGluGlnLysPheArgMetLeuSerGln	398
Db	1743	GCCAAAGAGAGGGGGAGCGCGGACAGAGAGCTGGAGAGGGAGCTACAGCACTCCAGAG	1802
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Qy	406	SerCysLysThrSerSerAsnAsnAsnSerMetValSerAsnThrLeuAlaLysMet---	424
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Qy	444	AspArgAlaSerGlnGlnGlnGlnThrAsnSerIleArgAsnTyrPheGlnProSerThr	463
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Qy	464	LysLysArgGluArgAspGluGluAsnGlnGluMetSerSerCysLysSerAlaArgIle	483
Db	2040	AAGCTGCACAGATGGAGAGGAGAACCCAGCAGCTGGAGGCTGAGAAAGGAG---GAGCTG	2096
Qy	484	GluThrSerCysSerLeuLeuGluGlnThrClnProAlaThrProSerLeuTrpLysAsn	503
Db	2097	AGGAAGAACGTGGATCTGTCTCAAG-----GCGCTGGGCAAGAAAG	2135
Qy	504	LysGluGlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnAsnLeuPhe	523
Db	2136	TCAGAGCGCTGGAGCTCAGCTACCAGCGTG-----AGCGCTGAGACCTCCGCG	2186
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Db	2187	CTGCAGCAGACGCTGGAG-----AGCAGCAGCCCAACAGACGAC	2225
Qy	544	LysLeuArgSerAsn-----LysLysArgGluMet	553
Db	2226	ACCTTGAGAGTGTAGCTGGCGGACGTGAGCGCTGAGCGCCAGCGCTGCGCGCGGACCTG	2285
Qy	554	AspAspValAlaIleGluAspGluValLeuGluGlnLeuPheLysAspThrLys-----	571
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Qy	572	-----ProGluLeuGluIleAspValLysValGlnLysGlnGluAspVal	587
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; Sequence 188, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Pearson, Cecelia I.
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: PA-0027-1 US
; CURRENT APPLICATION NUMBER: US/10/252,157
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,048
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: PERL Program
; SEQ ID NO 188
; LENGTH: 11167
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 261982.8
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 9131, 9138, 10638
; OTHER INFORMATION: a, t, c, g, or other
US-10-252-157-188

Alignment Scores:
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Score: 170.50 Matches: 122
Percent Similarity: 37.91% Conservative: 110
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QY	243	ValPheGlyGlyGlyGluAlaArgLeuIleThr---	253
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QY	254	GluGluAsnGluGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAspThr	273
DB	2853	GAAGAAGAAACAAGAGAGAGACTTTCTCTTCAGCAGAAGCGACAGTTGATAAAGACACG	2912
QY	274	GlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSerIle	293
DB	2913	ACCATCATGGAATTAAGAGATCGACTTCCT-----AAGAAGCAGCAAGCAAGTGCTTCC	2966
QY	294	MetAspMetLeuGlnArgGlnGly-----	303
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QY	304	ProIleProGluAlaGluIleGlyLeuAlaValIlePheMetThrThrLysAsnTyrCys	323
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QY	324	AspProGlnGlyHisProSerThrGlyLeuLysThrThrThrProGlyProSerLeuSer	343
DB	3045	-----GAAAGACGACCAAGCATCTCAAAACCAAAACA--TGTAAGAAAGTACAG	3089
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Job time : 713 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2004, 10:40:04 ; Search time 127 Seconds
(without alignments)
2620.495 Million cell updates/sec

Title: US-09-837-602-2
Perfect score: 3899
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Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs., 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	175	4.5	5661	US-08-938-105-2	Sequence 2, Appli
3	169	4.3	3384	US-08-923-992A-5	Sequence 5, Appli
4	166	4.3	8503	US-09-620-312D-130	Sequence 130, App
5	164.5	4.2	8948	US-09-643-597-119	Sequence 119, App
6	164.5	4.2	8948	US-09-480-884A-119	Sequence 119, App
7	164.5	4.2	8948	US-09-542-615A-119	Sequence 119, App
8	164.5	4.2	8948	US-09-606-421B-119	Sequence 119, App
9	163	4.2	8257	US-09-595-684B-30	Sequence 30, Appl
10	162.5	4.2	5857	US-09-220-132-79	Sequence 79, Appl
11	162	4.2	3135	US-09-107-532A-1575	Sequence 1575, Ap
12	161	4.1	3294	US-08-923-992A-7	Sequence 7, Appli

13	157.5	4.0	2672	3	US-09-214-564A-5	Sequence 5, Appli
14	157.5	4.0	2815	3	US-09-214-564A-1	Sequence 1, Appli
15	157	4.0	4200	1	US-08-242-932-1	Sequence 1, Appli
16	157	4.0	4200	1	US-08-714-481-1	Sequence 1, Appli
17	157	4.0	4200	5	PCT-US95-06111-1	Sequence 1, Appli
18	157	4.0	4200	3	US-09-104-324B-1	Sequence 1, Appli
19	156.5	4.0	3393	3	US-09-162-713-1	Sequence 1, Appli
20	156.5	4.0	3393	3	US-08-923-992A-9	Sequence 9, Appli
21	156	4.0	3492	3	US-08-630-822A-67	Sequence 67, Appl
22	155.5	4.0	1704	2	US-09-005-069-67	Sequence 26, Appl
23	155.5	4.0	1704	4	US-09-171-156A-26	Sequence 26, Appl
24	155.5	4.0	1704	4	US-09-004-730A-26	Sequence 26, Appl
25	155.5	4.0	1704	4	US-08-981-799A-26	Sequence 26, Appl
26	155.5	4.0	1704	4	US-09-134-001C-322	Sequence 322, App
27	155	4.0	30549	3	US-08-931-999-4	Sequence 4, Appli
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31	150.5	3.9	3063	4	US-08-468-024B-3	Sequence 12, Appl
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33	150.5	3.9	3063	4	US-09-599-652-1	Sequence 1, Appli
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38	150	3.8	1383	2	US-09-171-156A-28	Sequence 28, Appl
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42	149.5	3.8	2617	1	US-08-782-009-1	Sequence 1, Appli
43	149.5	3.8	2617	1	US-09-017-302-1	Sequence 1, Appli
44	149.5	3.8	2617	3	US-08-242-932-8	Sequence 8, Appli
45	147.5	3.8	3730	1	US-08-242-932-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-300-008B-1

; Sequence 1, Application US/09300008B

; Patent No. 6458534

; GENERAL INFORMATION:

; APPLICANT: Concannon et al.

; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE

; FILE REFERENCE: 9924-0003-228

; CURRENT APPLICATION NUMBER: US/09/300,008B

; CURRENT FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: US 60/083,269

; PRIOR FILING DATE: 1998-04-27

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 4386

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (26)...(2287)

US-09-300-008B-1

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Pred. NO.:

Score: 0

Percent Similarity: 3896.00

Best Local Similarity: 100.00%

Query Match: 99.87%

DB: 99.92%

US-09-837-602-2 (1-754) x US-09-300-008B-1 (1-4386)

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Qy 301 GlyLeuArgProIleProGluAlaGluIleGlyLeuAlaValIlePheMetThrThrLys 320
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 6, 2004, 10:40:04 ; Search time 127 Seconds

(without alignments)
2620.495 Million cell updates/sec

Title: US-09-837-602-2

Perfect score: 3899

Sequence: 1 MWKLLPAGGAGGEPYRLLT.....KESSLADLFRNPKRRR 754

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : 9

- Issued Patents NA:*
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 - 2: /cgcn2_6/ptodata/1/ina/5B.COMB.seq:*
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 - 5: /cgcn2_6/ptodata/1/ina/6C.COMB.seq:*
 - 6: /cgcn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3896	99.9	4386	4	US-09-300-008B-1
2	175	4.5	5661	4	US-08-938-105-2
3	169	4.3	3384	3	US-08-923-992A-5
4	166	4.3	8503	4	US-09-620-312D-130
5	164.5	4.2	8948	4	US-09-643-597-119
6	164.5	4.2	8948	4	US-09-480-884A-119
7	164.5	4.2	8948	4	US-09-542-615A-119
8	164.5	4.2	8948	4	US-09-606-421B-119
9	163	4.2	8257	4	US-08-595-684B-30
10	162.5	4.2	5857	4	US-09-220-132-79
11	162	4.2	3135	4	US-09-107-532A-1575
12	161	4.1	3294	3	US-08-923-992A-7

13	157.5	4.0	2672	3	US-09-214-564A-5	Sequence 5, Appli
14	157.5	4.0	2815	3	US-09-214-564A-1	Sequence 1, Appli
15	157	4.0	4200	1	US-08-242-932-1	Sequence 1, Appli
16	157	4.0	4200	1	US-08-714-481-1	Sequence 1, Appli
17	157	4.0	4200	3	US-08-923-992A-1	Sequence 1, Appli
18	157	4.0	4200	5	PCT-US95-08111-1	Sequence 1, Appli
19	156.5	4.0	3393	3	US-09-104-324B-1	Sequence 1, Appli
20	156.5	4.0	3393	3	US-09-162-713-1	Sequence 1, Appli
21	156	4.0	3492	3	US-08-923-992A-9	Sequence 9, Appli
22	155.5	4.0	1704	2	US-08-630-822A-67	Sequence 67, Appli
23	155.5	4.0	1704	2	US-09-005-069-67	Sequence 67, Appli
24	155.5	4.0	1704	4	US-09-171-156A-26	Sequence 26, Appli
25	155.5	4.0	1704	4	US-09-004-730A-26	Sequence 26, Appli
26	155.5	4.0	1704	4	US-08-981-799A-26	Sequence 26, Appli
27	155	4.0	30549	4	US-09-134-001C-322	Sequence 322, App
28	154.5	4.0	6755	3	US-08-931-999-4	Sequence 4, Appli
29	151	3.9	1830121	4	US-09-557-884-1	Sequence 1, Appli
30	151	3.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli
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36	150.5	3.9	5194	4	US-09-284-604-1	Sequence 1, Appli
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45	147.5	3.8	3730	1	US-08-242-932-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-300-008B-1
; Sequence 1, Application US/09300008B
; Patent No. 6458534
; GENERAL INFORMATION:
; APPLICANT: Concannon et al.
; TITLE OF INVENTION: A GENE ASSOCIATED WITH NIJMEGEN BREAKAGE
; FILE REFERENCE: 9924-0003-228
; CURRENT APPLICATION NUMBER: US/09/300,008B
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: US 60/083,269
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4386
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)...(2287)
US-09-300-008B-1

Alignment Scores:
Pred. No.: 0
Score: 3896.00
Percent Similarity: 100.00%
Best Local Similarity: 99.87%
Query Match: 99.92%
DB: 4
Length: 4386
Matches: 753
Conservative: 1
Mismatch: 0
Indels: 0
Gaps: 0

US-09-837-602-2 (1-754) x US-09-300-008B-1 (1-4386)

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RESULT 2

US-08-938-105-2
 ; Sequence 2, Application US/08938105
 ; Patent No. 6353151
 ; GENERAL INFORMATION:
 ; APPLICANT: Leinwand, Leslie A.
 ; APPLICANT: Vikstrom, Karen L.
 ; TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
 ; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheridan Ross P.C.
 ; STREET: 1700 Lincoln St., Suite 3500
 ; CITY: Denver
 ; STATE: CO
 ; COUNTRY: U.S.A.
 ; ZIP: 80203

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/938.105
 ; FILING DATE:

; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crook, Wanneil M.
 ; REGISTRATION NUMBER: 31,071
 ; REFERENCE/DOCKET NUMBER: 3595-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 863-9700
 ; TELEFAX: (303) 863-0223
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5661 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..5661

US-08-938-105-2

Alignment Scores:
 Pred. No.: 4.76e-08 Length: 5661
 Score: 175.00 Matches: 102
 Percent Similarity: 37.98% Conservative: 67
 Best Local Similarity: 22.92% Mismatches: 141
 Query Match: 4.49% Indels: 135
 DB: 4 Gaps: 19

US-09-837-602-2 (1-754) x US-08-938-105-2 (1-5661)

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 Qy 346 ValSerValAspGluLysLeuMetProSer-AlaProValAsnThrThrTyrValAl 365
 Db 2325 TTGCCGTGGATGAAGCTCTACTCAAGATCAAGCCGCTGCTGAAGAGC-----GC 2375
 Qy 365 aAspThrGluSerGlnGlnAlaAspThrTrpAspLeuSerGluArgProLys----- 382
 Db 2376 AGACACAGAGAAGGAGATGGCCACATGAAGAGAGAGTTCCGGCGAGTCAAGATGCAC 2435
 Qy 383 -----GluLeuLysValSerLysMetGluGlnLysPheArgMetLeuSerGlnAs 399
 Db 2436 AGAGAAGTCTGAGGCTCGCCCGCAAGGAGCTGGAGGAGAAGATGGTGTCTGCTGCAGGA 2495

Qy 399 pAlaProThrValLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAs 419
 Db 2496 GAAGAATGACCTGCAGCTCCAAGTGCAGCGGCAACAAGACAC- 2538
 Qy 419 nThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerI 439
 Db 2539 -----CT 2540
 Qy 439 eAsnLysSerLysAspArgAlaSerGlnGlnGlnThrAsnSerIleArgAsnTyrPh 459
 Db 2541 GGCAGATGCCGAGGAGCGCTGCCACCAG-----CTGATCAAGACACAGAT 2585
 Qy 459 eGlnProSerThrLysLysArg-----GluArgAspGluGluAsnGlnGluMetSe 476
 Db 2586 CCAGCTGGAGGCCAAGGTGAAGGAGATGACCGAGAGCTCGAGGACGAGGAGGAGATGAA 2645
 Qy 476 r-----SerCysLysSerAlaArgIleGluThrSerCysSer---LeuLeuGluG 492
 Db 2646 CGCCGAGCTCACGCCCAAGAGCGCAAGCTGGGAAGACGAGTGTCTCAGAGCTCAAGAAGA 2705
 Qy 492 nThrGlnProAlaThrProSerLeuTyrLys---AsnLysGluGlnHisLeuSerGluAs 511
 Db 2706 TATCGATGACCTGGAGCTGACCTGGCCAGAGTGGAGAGAAAGAACGACCGACACAGAGA 2755
 Qy 511 nGluProValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLysSerI 531
 Db 2766 CAAG-----GTTAAAAACCT 2780
 Qy 531 eValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLys-- 550
 Db 2781 GACAGAGGAGATGCCCGGCTGGACGACGAGATCATTTGCCAAGCTCACCAGGAGAGAAAGC 2840
 Qy 551 -----ArgGluMetAspAspValAlaIleGluAspGluValLeuG 564
 Db 2841 TCTTCAAGAGGCCACGACGAGCCCTGATGATGACCTTCAGGCTGAGGAGACAAAGGTCAA 2900
 Qy 564 uGlnLeuPheLysAspThrLysProGluLeuGluIleAspValLysValGlnLysGlnG 584
 Db 2901 CACACTG-----ACCAAGTCTAAAGTCAAGCTGGAGCAGCAGCTGGATGATCGGA 2951
 Qy 584 uGluAspValAsnValArgLysArgProArgMetAspIleGluThrAsnAspThrPheSe 604
 Db 2952 GGGATCCCTGGAGCAGGAGAAGAGTGGCATGGACCTGGACGCA----- 2997
 Qy 604 rAspGluAlaValProGluSerSerLysIleSerGlnGluAsnGluIleGlyLysLysAr 624
 Db 2998 -----GCAAAAGCG 3005
 Qy 624 gGluLeuLysGluAspSerLeuTrpSerAlaLysGluIleSerAsn-----AsnAspLy 642
 Db 3006 GAAGCTGGAGGGTGACCTGAAGCTGACCCAGGAGAGCATCATGGACCTGGAGAACGACAA 3065
 Qy 642 sLeuGlnAspAspSerGluMetLeuProLysLysLysLeuLeuThrGluPheArgSerLe 662
 Db 3066 GCTTCAG-----CTGGAGGAAAAAGCTCAAGAAGAAAGAGTTT----- 3102
 Qy 662 uValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGly---G 681
 Db 3103 -----GACATCAGTCAGCAAGACAGTAAATATAGAGCAGGACGAGCCCTGGC 3149
 Qy 681 nLeuLysAsnPhelLysLysPheLysLysValThrTyrProGlyAlaGlyLysLeuProH 701
 Db 3150 CCTTCAGCTCAGAGAACTGAAGGA----- 3177
 Qy 701 sIlelleGlyGlySerAspLeuIleAlaHisHisAlaArgLysAsnThrGluLeuGluG 721
 Db 3178 -----AACCGAGCGCGCATCGAGGAGCTGGAGGA 3206
 Qy 721 uTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluGluSerLeuAlaAs 741
 Db 3207 GGAGCTAGAGCGGAG-----CGCACGCCCGCGGCAAGGTGGAGAGCTGCGCTC 3257

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QY 741 pAspLeuPheArg 745
 Db 3258 AGACCTGACCCGG 3270

RESULT 3
 US-08-923-992A-5
 ; Sequence 5, Application US/08923992A
 ; Patent No. 6280738
 ; GENERAL INFORMATION:
 ; APPLICANT: Tai, Joseph Y.
 ; APPLICANT: Blake, Milan S.
 ; TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B
 ; TITLE OF INVENTION: Streptococcal Beta Antigens
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 ; STREET: 1100 New York Avenue, N.W., Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/923,992A
 ; FILING DATE: 05-SEP-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/024,707
 ; FILING DATE: 06-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Esmond, Robert W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3384 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3384
 ; US-08-923-992A-5

Alignment Scores:
 Pred. No.: 8.99e-08 Length: 3384
 Score: 169.00 Matches: 142
 Percent Similarity: 37.45% Conservative: 125
 Best Local Similarity: 19.92% Mismatches: 238
 Query Match: 4.33% Indels: 208
 DB: 3 Gaps: 38

US-09-837-602-2 (1-754) x US-08-923-992A-5 (1-3384)

QY 192 GlnIleGluSerPheTyrProLeuAspGluProSerIleGlySerLysAsnValAsp 211
 Db 283 CAGAAAAATGAGTTTAAACAAAAAATTCATGAAACAAATGATTCGTGATTCATTATAGAA 342

QY 212 LeuSerGlyArg 402
 Db 343 TTAGAAATCAATTTACGAACTAATAGACTGTTACACATCAACAACTAGAGAGTT 402

QY 222 PheLysGlyLysThrPheIlePheLeuAsnAlaLysGlnHisLysLysLeuSerAla 241
 Db 403 GAGAAAGATAAG-----AAAGCTAAGCAACAGAAACCTCTGAAACAGTCA 447

QY 242 ValValPheGlyGlyGluAlaArgLeuIleThrGluGluAsnGluGluHisAsn 261
 Db 448 -----GATACGAAGTAGATCTAGCAATATTGCAAGAGAGCTTAAT 489

QY 262 PhePheLeuAlaProGlyThrCysValValAsp---ThrGlyIleThrAsnSerGlnThr 280
 Db 490 CATCAAAAAAGTCCAGTTGAAAAAATGCGACCAAGGGAATCACAATGAAGAT--- 546

QY 281 LeuIleProAspCysGlnLysLysTrpIleGlnSerIleMetAspMetLeuGlnArgGln 300
 Db 547 -----AAAGATTCTATGCTGAAAAAATCGAAGATATTCGTAACAAGCTCAACAAGCA 600

QY 301 GlyLeuArgProIleProGluAlaGluIle-----GlyLeuAlaValIlePheMetThr 318
 Db 601 GATAAAAAAGCAAGATCCGGAAGTTGTAAGAACTAGGTAAACTCTTTAGTTC 660

QY 319 ThrLysAsnTyrCysAspProGlnGlyHisProSerThrGlyLeuLysThrThrPro 338
 Db 661 ACTAAAGCTGGTCTGGATCAAGAAATTCATGACATGTGAAGAAAGAACGAGT----- 714

QY 339 GlyProSerLeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaProVal 358
 Db 715 -----AGTGAGGAAATATCTCAGAAAGTTGATGAACACTAT-----GCT 753

QY 359 AsnThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeuSer 378
 Db 754 AATAGCCTTCAGAACCTTCTCTCAAAATCTCTTGAAGAACTAGATGAAGCACTACCAAT 813

QY 379 GluArgProLysGluIleLysValSerLysMetGlu-----GlnLys----- 392
 Db 814 GAAACAGCTACACAGTTAAATAATCAATTTAGAAAAACGCTCAAAAGCTCAAGAAATG 873

QY 393 -----PheArgMetLeuSerGlnAspAlaPro 401
 Db 874 CAACCTCTTATCAAGAAACGAATGTGAATGTATAGGCTATAGTGAGAGCTTGGAG 933

QY 402 ThrValLysGluSerCysLysThrSerSerAsnAsn-----SerMetValSerAsn 419
 Db 934 CAGTTTGAGAGGAATTAACATAATTCGGAAGCTAATTAGAAAGTTGGTGGCAA 993

QY 420 ThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLys---LeuProSer 438
 Db 994 TCTAAAGAAATCGTAAGAGAATACGAAGGAAACTTAATCAATCTATAAATCTTCCAGAA 1053

QY 439 IleAsnLysSerLysAspArgAlaSerGln-----GlnGlnGlnThrAsnSerIleArg 456
 Db 1054 TTAAGCAACTAGAGAGGAGCTCATTGGAAGTTGAAACAAAGTTGTGAGGATTTTGA 1113

QY 457 AsnTyrPhe-----GlnProSerThrLysLysArg---GluArgAsp----- 469
 Db 1114 AAAAAATTTAAACGTCAGAGCAAGTCACACCAAAAAACGTCACAAACGAGTTAGCT 1173

QY 470 -----GluGluAsnGlnGluMetSerCysLysSerAlaArgIleGluThrSerCys 487
 Db 1174 GCTAATGAAAAATAATCAACAA-----AAGATTGAGTTAACAGTT 1212

QY 488 SerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTyrLysAsnLysGluGlnHis 507
 Db 1213 TCA-----CCAGAGAATATCATCTGATATGGAAGGTGAAGACGCTGAA 1254

QY 508 LeuSerGluAsnGluProValAspThrAsnSerAspAsnLeuPheThrAsp---Thr 526
 Db 1255 TTATCA-----GTCACAGCTAAAGAGTATTCGACAGCAGCGTTGGACTTCAGT 1302

QY 527 AspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArg 546
 Db 1303 GATCTT-----TTACAAAATATAATTCGTCGTGTATCA-----CATAGATTAGT 1347

QY 547 SerAsnLysLysArgGluMetAspValAlaIleGluAspGluValLeuGluGlnLeu 566
 Db 1348 ACAATTTAAGCACTAAACCGGATTAATCATAGATTGCCAAATCTACTATCAAGAAATTG 1407

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489 AATATACANTGAACCATTACAGATTACTCTGTGGCAGCTCAAAAAATGAAACCTTTAAT 548
 176 rPheThrGluPheLeuLysAlaValGlnSerLysLysGlnProProGlnIleGluSerPh 196
 549 TATTCGAGAAGATGCTCAATAGG-----AATGTGTA 578
 196 eTyProProLeuAspGluProSerIleGlySerLysAsnValAspLeuSerGlyArgGI 216
 579 TGTTGCTGATCTCACAGAAGAAGTGTATATATCATCAGAAATGCCTTTG----- 627
 216 nGluArgLysGlnIlePheLysGly---LysThrPheIlePheLeuAsnAlaLysGlnHi 235
 628 -----AAATGATTACAAAGGGAGAAAAGACGCAGCATATCGAGAAACAAAAATGAA 680
 235 sLysLysLeuSer---SerAlaValValPheGlyGlyGluAlaArgLeuIleThrGI 254
 681 TCAGAAGACAGFCGTTCTCATACCATCTTT-----AGGATGATTTTGG 725
 254 uGluAsnGluGluGluHisAsnPheLeuAlaProGlyThrCys----- 266
 726 AAGCAGAGAGAGGGTGAA-----CCTTCTAATGTGAAGATCTGTTAA 770
 270 -----valValasp-----ThrGlyII 275
 771 GGTATCCCATTTGAATTTGGTTGATCTTGCGAGCAGTGAAGAGAGCTGCTCAAACAGCGCG 830
 275 eThrAsnSerGlnLeuIleProAspCysGlnLysLysTrpIleGlnSerIleMetAS 295
 831 TGCAGGTGTCGG--CTCAAGGAGCTGTAA-----ATAAATCGAAGCTTATT 878
 295 pMetLeuInArgGlnGlyLeuArgProIleProGluAlaGluIleGlyLeuAlaValII 315
 879 TATTTTG---GGACAAGTGATCAAGAAACTTAGTGATGGACAAGTTGGTGGTTTCATA-- 933
 315 epHeMetThrThrLysAsnTyrCysaspProGln----- 326
 934 -----AATATATCGAGATACGAAGTTAACACGAATTTCTTCAGAAATTCCTT 977
 327 ---GlyHisProSerThrGly---LeuLysThrThrProGlyProSerLeuSerGI 344
 978 GGGAGGAATCCAAACACACGATATTATCTGCACAATTACTCCA----- 1020
 344 nGlyValSerValAspGluLysLeuMetProSerAlaProValAsnThr----- 360
 1021 ----GPATCTTTTGATGAACACTCTTACTGCTCCAGTTTGCACGACTCTCTAAATATAT 1076
 361 -----ThrThrTyValAlaAspThrGlusergluGlnAla----- 372
 1077 GAAGAATACTCCTTATGTTAATGAGGTATCACTGATGAAGCTCTCTGAAAAGGTATAG 1136
 373 ---AspThrTrpAspLeuSerGluArgProLysGluIleLysValserLysMetGluGI 391
 1137 AAAAGAAATAATGGATCTTAAAAAACAATATAGAGGAGTT-----TCITTTAGAGAC 1187
 391 nLysPheArgMetLeuSerGlnasp-----AlaProThrValLysGluSerCysLysTh 409
 1188 GGCGGCTCAGGCATCGAAAAGAACCAATTTGGCCCAACTTTTGGAGAAAAGAGTTTGGCT 1247
 409 rSerSerAsnAsnSerMetValSerAsnThrLeuAlaLysMetArgileProAsnTy 429
 1248 TCAGAAAAGTACAGAATGAGAAAATTGAAAAC---TTAACACGGATGCTGTGACCTTCTC 1304
 429 rGlnLeuSerProThrLys-----Le 436
 1305 TTCCCTTCAGGTCACACGGAATTAAGGCTAAAGAAAACGAGAGTTACTTTGGTGCCT 1364
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 1365 TGGCAAAATTAACAAAATGAGAAC---TCAACTATGAGATCAATTTAATATACCAAC 1421
 456 gAsnTyPheGlnProSerThrLys-----LysArgGluargAspGluGI 471
 1422 AAATATAACACAAAAACACATAAGCTTTCTATAAATTTATTACGAGAATTCATGAATC 1481

Qy	471	uAeGlnGluMetSerCysSerAlaArglleGluThrSerCysSerLeuLeuGl	491
Db	1482	TGTCGTGCAGCTCTGATCTTTTCAGTACACTCTTGATACATTAAGTCGAGATA----	1536
Qy	491	uGlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGluGlnHisLeuSerGluAs	511
Db	1537	-GAATGGAAATCCAGCAACAAAGCTACTA-----AATCAGGAGAATATAGAAAGTGAAGTT	1589
Qy	511	nGluProValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLysSerIl	531
Db	1590	GAACCTCACCTTCGTGCTGACTATGATAATCTGGTATTAGACTATGAACAACACTCGAACAGA	1649
Qy	531	eValLysAsnSerAlaSerLysSerHisAlaLaGluLysLeuArgSerAsnLysLysAr	551
Db	1650	AAAAAATAAATAATG-----GAATTGAAATTAATAAGAAAGAA	1685
Qy	551	gGluMetAspAspValAlaIleGluAspGluValLeuGluGlnLeuPheLysAspThrLy	571
Db	1686	TGATTTGGAT-----GAATTTGAGGCTCTAGAAAGAAACTATAAAGAGATCA	1733
Qy	571	sProGluLeuGluIleAspValLysValGlnLysGlnGluAspValAsnValArgLy	591
Db	1734	A---GAGATGCAACTAATTCATGAAATTTCGAACTTTAAAGAAATTTAGTAAAGCATCGAGA	1790
Qy	591	sArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaValProGluSe	611
Db	1791	AGTATATATCAAGATCTT-----	1809
Qy	611	rSerLysIleSerGlnGluAsnGluIleGlyLysLysArgGluLeu-----LysGl	628
Db	1810	-----GAGATGAACTCAGTTCAAAGGTAGACTGCTGCTTAGAGAAAGGA	1853
Qy	628	uAspSerLeuTrpSerAlaLysGluIleSerAsnAsnAspLysLeuGlnAsp-----	645
Db	1854	AGACCAGATTAAAGAGCTACAGGAATACATAGACTCTCAAAAGCTAGAAATATAAAAT	1913
Qy	646	-----AspSerGluMetLeuProLysLysLeuLeuLeuLeuThrGluPh	659
Db	1914	GGACTTGTCATACTATTGGAAAGCAATTGAAGACCCAAACAAATGAAGCAGACTCTGTT	1973
Qy	659	eArgSerLeuValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAsp--	678
Db	1974	TGATGCTGAAACTGTAGCCCTTGATGCCAAGAGAAATCAGCCCTTTCTTAGAAGTGAAA	2033
Qy	679	-----TyrGlyGlnLeuLysAsn--	684
Db	2034	TCTGGAGTTCAAGGAGAAAATGAAGAAGCTTGCAACTACATACAGCAATGGAAAATGA	2093
Qy	684	-----	684
Db	2094	TATTCAGTTATCAAGCCAAATTGGAGCAAAAAGAAAATGCAAGTTGATCTGGAGAA	2153
Qy	685	-----PheLysLysPheLysLysValThrTyrProGlyAlaGlyLysLe	699
Db	2154	AGAATTACAATCTGCTTTAATGAGATAACAAAACTCACTCCCTTTATAGATGCGAAAGT	2213
Qy	699	uProHisIleIleGlyGlySerAspLeuIleAlaHis-----HisAlaArgLysAsnTh	717
Db	2214	TCCA-----AAAGATTGCTGCTGTAATTTGGAAATTGGAAGGAAGATTAC	2258
Qy	717	rGluLeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluGl	737
Db	2259	TGATCTTCAGAAAGAACTAAATAAGAAGTTGAA---GAANAATGAAGCTTTCGGGAAGA	2315
Qy	737	u	737
Db	2316	A	2316

RESULT 5
US-09-643-597-119
; Sequence 119, Application US/09643597
; Patent No. 6426072


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Qy 459 ----- 459
Db 3755 ACTCGAAGACGAGCAATGTGAAAGAGGAACTTTGGTTGGCAGAAATTAGAGTCTGA 3814
Qy 460 -----GlnPr 461
Db 3815 GAAAGCCATCAAGAGAGAGTACGAGATTGAAAGGTTGAGGGTTCTACTGCAGGAAGA 3874
Qy 461 oSerThrLysLysArgGluArgGluGlu-----AenGl 473
Db 3875 AGGACCCGGAAGAGAAATATGAAATGAGCTGGCAAGGTAGAAACCACTATAATGA 3934
Qy 473 nGluMetSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuGluGlnTh 493
Db 3935 GGAGATGAGTAATTTAAGAAC--AAGTATGAACAGAGATTAAACATTACGAAGACCAC 3991
Qy 493 rGlnProAlaThrProSerLeuTrpLysAsnLysGluGlnHisLeuSerGluAsnGluPr 513
Db 3992 CATCAAGGAGATA---TCCATGCAAAAAGAGGATGATTCCAAAATCTTAGAAACCAAG-- 4046
Qy 513 oValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLys---SerIleVa 532
Db 4047 -CTTGATAGACTTTCAAGGGAAAT-----CGAGATCTGAAGGATGAAATTGT 4093
Qy 532 lLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLysArgG1 552
Db 4094 CAGGCTCAATCACAGCATCTTGCAGGCCACTGAGCAGCGAAGCGAGCTGAAGAAACGC 4153
Qy 552 uMetAspAspValAlaIleGluAspGluValLeuGlnLeuPheLysAspThrLysPr 572
Db 4154 CCTTCAGCAAAAGCCCTGTGGCTCTGAGATAATCGAAG-----AAGCA 4198
Qy 572 oGluLeuLeuLeuAspValLys---ValGlnLysGlnGluLeuAspValAsnValArgLy 591
Db 4199 GCATCTGGAGATAGAACTGAAGCAGGTCATGCAGCAGCGCTCTGAGCAATGCCCGCA 4258
Qy 591 sArgProArgMetAspIleGluThrAsnAspThr----- 602
Db 4259 CAACGAGTCCCTGGAG--GAGGCTGCCAAGACCATTCAGGACAAAATAAGGAGATCGA 4315
Qy 603 -----PheSerAspGluAlaValProGluSerSerLysLysSerGlnGl 617
Db 4316 GAGACTCAAGCTCAGTTTTTCAGGAGGAGGCC-----AAGCGCGCTGGGAATATGA 4366
Qy 617 uAsnGluIleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLys----- 635
Db 4367 AAATGAATGTAGTAAGTAAGAAACAATTATGATGAGGAGATCATTTAGCTTAAATAATCA 4426
Qy 635 ----- 635
Db 4427 GTTTGAGACCGAGATCAACATCACCAAGACCACCATCCACGAGCTCACCAGCAGGA 4486
Qy 636 -GluIleSerAsnAsnAspLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLe 655
Db 4487 AGAGATACCACTGGCTACCGGGCTCAGATAGACAATCTACCCGAGAAAAACAGGAGCTT 4546
Qy 655 uLeuThrGluPheArgSerLeuValIleLysAsnSer-----ThrSerArgAsnPr 672
Db 4547 ATCTGAAGAAATAAAGAGGCTG-----AAGAACACTCTAACCCAGACCCACAGAGAATCT 4600
Qy 672 oSerGlyIleAsnAspAspTyrrGlyGlnLeuLysAsnPhelLysLysPheLysValTh 692
Db 4601 CAGGAGGGTGGAGAGACATCCACAG-----CAAAAGGCCAC 4639
Qy 692 rTyProGlyAlaGlyLysLeuProHisIleIleGlySerAspLeuIleAlaHisHi 712
Db 4640 T-----GGCTCTGAGGTG----- 4652
Qy 712 sAlaArgLysAsnThrGluLeuGluGluTrpLeuArgGln-----GluMetGluValGl 730
Db 4653 -TCTCAGAGGAAACAGCAGCTGGAGGTGAGCTGAGCAAGTCACTCAGATGCGAACAAGA 4711
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Qy 730 nAsnGlnHisAlaLysGluGluSerLeuAlaAsp 741
Db 4712 GGAGAGCGTAAGATATAAGCAATCTCTTGATGAT 4745

RESULT 6
US-09-480-884A-119
; Sequence 119, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Pan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480, 884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 119
; LENGTH: 8948
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-480-884A-119

Alignment Scores:
Pred. No.: 1,44e-06 Length: 8948
Score: 164.50 Matches: 187
Percent Similarity: 34.23% Conservative: 132
Best Local Similarity: 20.06% Mismatches: 295
Query Match: 4.22% Indels: 319
DB: 4 Gaps: 45

US-09-837-602-2 (1-754) x US-09-480-884A-119 (1-8948)
Qy 2 TrpLysLeuLeuProAlaAlaGlyProAlaGlyGlyGluProTyrrArgLeuLeuThrGly 21
Db 2331 TGGATGCTGATG-----GAGCTGCAGAAAGATTCCGAGGCAG 2366
Qy 22 ValGluTrpValValGlyArgLysAsnCysAlaIleLeuLeuGluAsnAspGlnSerIle 41
Db 2367 ATAGAGCAGCTCGCAGGCGAGGATGACTCTCAAAACCTCTTAGCAGCCAGGGG--- 2423
Qy 42 SerArgAsnHisAlaValLeuThrAlaAsn-----PheSerValThrAsnLeuSerGln 59
Db 2424 TCTTCTCACCACATCATCAGTGAGAAATTAACAGCTTAAGAGTGTGCAGATGATTCACAA 2483
Qy 60 ThrAspGluIleProValLeuThrLeuLysAspAsnSerLysTyrrGlyThrPheValAsn 79
Db 2484 GCAATTGCTGAGGTCTCTCAACCAGCTTAAAGAT-----ATGCTTGCCAACCTTCAGAGGT 2537
Qy 80 GluGluLys-----MetGlnAsn-----GlyPheSerArgThrLeuLysSer 93
Db 2538 TCTGAAAGTACTGCTATTATACAGAATGAAGTATTTGGACTATTTCAGAACTCGAAAT 2597
Qy 94 GlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrrGluProLeu 113
Db 2598 ATCAATGGTGTACAGATGGCTACTTAATAGCTTATGACAGTAAGG----- 2645
Qy 114 ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaIleLeu 133
Db 2646 -----GCACCTGCTCCAGGCTATTCTC 2666
Qy 134 GlnLeuGlyGlyPheThrValAsnAsnTrpThrGluGluCysThrHisLeuValMetVal 153
Db 2667 CAA-----ACAGACACATG-----TTAAAGGTTTAT 2693
Qy 154 SerValLysValThr-----IleLysThrIleCys-----AlaLeu 165
Db 2694 GAAGCCAGGCTCACTGAGGAGGAACTGTCTGCTGACCTGGATAAAGTGAAGCTTAC 2753
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Db 4653 -TCTCAGAGAAACAGCAGCTGGAGGTGTGAGTGCAGACAAAGTCACCTCAGATGCGAAGCAGA 4711
 Qy 730 nAsnGlnHleAlaLysGluGluSerLeuAlaAsp 741
 Db 4712 GGAGAGCETAAGATATAAGCAATCTCTTGATGAT 4745

RESULT 7

US-09-542-615A-119
 ; Sequence 119, Application US/09542615A
 ; Patent No. 6518256
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy A.
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.455C8
 ; CURRENT APPLICATION NUMBER: US/09/542.615A
 ; CURRENT FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 350
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 119
 ; LENGTH: 8948
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-542-615A-119

Alignment Scores:

Pred. No.: 1.44e-06 Length: 8948
 Score: 164.50 Matches: 187
 Percent Similarity: 34.23% Conservative: 132
 Best Local Similarity: 20.06% Mismatches: 295
 Query Match: 4.22% Indels: 319
 Gaps: 45

US-09-837-602-2 (1-754) x US-09-542-615A-119 (1-8948)

Qy 2 TrpLysLeuLeuProAlaAlaGlyProAlaGlyGluProTyrArgLeuLeuThrGly 21
 Db 2331 TGGATGCTGATG-----GAGCTGCAGAGAAATTCGCGAGCAG 2366
 Qy 22 ValGluTyrValValGlyArgLysAsnCysAlaLeuLeuGluAsnAspGlnSerIle 41
 Db 2367 ATAGAGCCTGGCGGCGAGGATGACTCTCAAAAACCTCCCTCTAGCAGACCGGG--- 2423
 Qy 42 SerArgAsnHisAlaValLeuThrAlaAsn-----PheSerValThrAsnLeuSerGln 59
 Db 2424 TCTTCTCACCACATCACAGTGAATTAACGAGCTTAAGAGTGTGCAGAAATGATTTCACAA 2483
 Qy 60 ThrAspGluIleProValLeuThrLeuLysAspAsnSerLysTyrGlyThrPheValAsn 79
 Db 2484 GCAATTGTGCTGAGTTCTCAACAGCTTAAAGAT-----ATGCTTGCACCACTTCAGAGGT 2537
 Qy 80 GluGluLys-----MetGlnAsn-----GlyPheSerArgThrLeuLysSer 93
 Db 2538 TCTGAAAGTACTGCTATTTCACAGATGAAGTATTGGACTATTTCAGAACTGGAAT 2597
 Qy 94 GlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrGluProLeu 113
 Db 2598 ATCAATGGTGTACAGATGGCTACTTAAATAGCTTATGCACAGTAAG----- 2645
 Qy 114 ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaLeu 133
 Db 2646 -----GCACCTGCTCCAGGCTATTCTC 2666
 Qy 134 GlnLeuGlyGlyPheThrValAsnAsnTrpThrGluGluCysThrHisLeuValMetVal 153
 Db 2667 CAA-----ACAGAGACATG-----TTAAGGTTTAT 2693
 Qy 154 SerValLysValThr---IleLysThrIleCys-----AlaLeu 165

Db 2694 GAAGCCAGCTCACTGAGGAGGAAACTGTCTGCTGGACCTGGATAAAAGTGAAGCTTAC 2753
 Qy 166 IleCysGlyArgProIleValLysProGlu----- 175
 Db 2754 CGCTGTGGACTGAAGAAATAAATAATGACTTGAACCTGGAAGAAGTCGTTGTGGCACT 2813
 Qy 176 TyrPheThrGluPheLeuLysAlaValGlnSerLysLysGlnProProGlnIleGluSer 195
 Db 2814 ATGAACAGACAACCTACAGAAAGCCAGCAGATCCACTCTCAGACTTCACAGCAGTATCCA 2873
 Qy 196 PheTyrProProLeuAspGluProSerIleGlySerLysAsnValAspLeuSerGlyArg 215
 Db 2874 CTTTAT---GATCTGACTTGGCGCAAGTTCGGTGAATAAGTCAACAGCTGACAGACCGC 2930
 Qy 216 GlnGluArg-----LysGlnIlePhe 222
 Db 2931 TGGCAAGGATAGATAAACAGATCGACTTTAGATTATGGACCTGGAGAAACAATCAAG 2990
 Qy 223 LysGlyLysThrPhe-----IlePheLeuAsnAla 232
 Db 2991 CAATTGAGGAATTATCGTGATAACTATCAGGCTTTCTGCAAGTGGCTCTATGATCGTAA 3050
 Qy 233 LysGlnHisLysLysLeuSerSerAlaValPheGlyGlyGluAlaArgLeuIle 252
 Db 3051 CGCCGCGAGGATTCCTTAGAATCCATGAAATTT---GGAGATTCCAAACACAGTC 3101
 Qy 253 ThrGluGluAsnGluGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAsp 272
 Db 3102 ATCGGTTTTGTAATGAGCAGACAAGAACTTG----- 3131
 Qy 273 ThrGlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSer 292
 Db 3132 -----CACAGTGAATATCTGGCAACGAGACAAATCAGAGGAAGTACAAAA 3179
 Qy 293 IleMetAspMetLeuGlnArgGlnGlyLeuArgProIleProGluAlaGluIleGlyLeu 312
 Db 3180 ATTGCTGAACCTTTCGCGCAATTCA-----ATTAAAGATTATGAGCTCCAGCTG 3227
 Qy 313 AlaValIlePheMetThrThrLysAsnTyrCysAspProGlnGlyHisProSerThrGly 332
 Db 3228 GCC-----TCATAC-----ACCTCAGGA 3245
 Qy 333 LeuLysThrThrThrProGlyPro-----SerLeuSerGlnGlyVal 346
 Db 3246 CTGGAACCTCTGCTGAACATACCTATCAAGAGGACCATGATTTCAGTCCCTCTTGGGGTG 3305
 Qy 347 SerValAspGluLysLeuMetProSerAlaProValAsnThrThrThrThrValAlaAsp 366
 Db 3306 ATTCTGCAAGAGGC-TGCAGATGTTTCATGCTCGGTACATTGAACACTACTTAC----- 3355
 Qy 367 ThrGluSerGluGlnAlaAspThrTip-Asp-----LeuSerGluArgProLys 382
 Db 3356 -----AAGATCTGGAGACTATTACAGGTTCTTAAGTGAGATGCTGAA 3397
 Qy 382 sGluIleLysValSerLysMetGluGln-----LysPheArgMetLeuSerGlnAspAlaPr 401
 Db 3398 GAGTTTGGAAAGTCTGAAGCTGAAAAATACCAAGATCGAAGTTTGGAGAGGAGCTCAG 3457
 Qy 401 oThrValLysGluSerCysLysThrSerSerAsnAsnAsnSerMetValSerAsnThrLe 421
 Db 3458 ACTGCCCGGAGATGCCAACTCGGAAAACTGTAAATAAGAACAAATTCCTGGATCAGAACCT 3517
 Qy 421 uAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLysLeuProSerIleAsnLys 441
 Db 3518 GCAGAAATACAGCAGAGTGTCCCGATTCAAA---GCGAAGCTTCGAGCCTGGAGGA 3574
 Qy 441 sSerLysAspArgAla----- 446
 Db 3575 GCTGAAGAGACAGGCTGAGCTGGATGGAGAGTCGGCTAAGCAAAATCTAGACAAAGTGCTA 3634
 Qy 447 -----SerGln 448

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Db 3635 CGGCCAAATAAAGAACTCAATGAGAGAGATCACCGACTGACTTATGAGATTGAGATGA 3694
Qy 448 nGlnGlnGlnThrAsnSerIleArgAsnTyrPhe----- 459
Db 3695 AAAGAGAAGAGAAAATCTGTGGAAGACAGATTTGACCAACAGAGAAGATGACTATGACCA 3754
Qy 459 ----- 459
Db 3755 ACTGAGAAACAAAGCAATCTGAAAGAGAGAACCTTGGTTGGCAGAAATTAGAGTCTGA 3814
Qy 460 -----GlnPr 461
Db 3815 GAAAGCCATCAAGAGAAAGAGTAGCAGATTTGAAAGGTTGAGGGTTCTACTGCGAGGAGA 3874
Qy 461 oSerThrIlyslsArgGluArgAspGluGlu-----AsnG1 473
Db 3875 AGGCACCGGAGAGAGAAATATGAAATGAGCTGCGAAAGGTAAAGAACCACTATATGA 3934
Qy 473 nGluMetSerSerCysIysSerAlaArgIleGluThrSerCysSerIleuLeuGluGlnTh 493
Db 3935 GGAGATGAGTAATTTAAGGAAC---AAGTATCAAAACAGAGATTAAACATTACGAAGACCAC 3991
Qy 493 rGlnProAlaThrProSerLeuTrpIysAsnIysGluGlnHisLeuSerGluAsnGluPr 513
Db 3992 CATCAAGAGATA---TCCATGCAAAAGAGAGATGATTCAAAATCTTGAAGAACCGAG-- 4046
Qy 513 oValAspThrAsnSerAspAsnLeuPheThrAspThrAspLeuLys---SerIleVa 532
Db 4047 -CTTGATAGATTTCAGGGGAAT-----CGAGATCTGAAGGATGAATGT 4093
Qy 532 lIysAsnSerAlaSerIysSerHisAlaAlaGluLysLeuArgSerAsnIysLysArgG1 552
Db 4094 CAGGCTCAATCAGCAGCATCTTCAGGCCACTGAGCAGCGAAGCGAGCTGAAGAAACGC 4153
Qy 552 uMetAspAspValAlaIleGluAspGluValLeuGluGlnLeuPheIysAspThrLysPr 572
Db 4154 CCTTCAGCAAAAGCGCTGTGCTCTGAGATAATCGAAG-----AAGCA 4198
Qy 572 oGluLeuGluIleAspValLys---ValGlnIysGlnGluAspValAsnValArgLy 591
Db 4199 GCATCTGGAGATAGACTGAGAGCAGGTCTATCGCAGCGGCTCTGAGGACATGCCGGCA 4258
Qy 591 sArgProArgMetAspIleGluThrAsnAspThr----- 602
Db 4259 CAAGCAGTCCTCGAG---GAGGCTGCCAAGACCATTCAGGACAAAATAAGGAGATCGA 4315
Qy 603 -----PheSerAspGluAlaValProGluSerSerIysIleSerGlnG1 617
Db 4316 GAGACTCAAGCTGAGTTTTCAGGAGGAGGCC-----AAGCGCCGCTCGGGAATATGA 4366
Qy 617 uAsnGluIleGlyLysLysArgGluLeuLysGluAspSerLeuTrpSerAlaLys----- 635
Db 4367 AAATGNACTGATAGGTAAAGAAACAATTATGATGAGGAGATCATAGCTTAAAAAAATCA 4426
Qy 635 ----- 635
Db 4427 GTTTGAGACCGAGATCAACATCACCAAGACCACCATCCAGCTCACCATGCAGAAAGGA 4486
Qy 636 -GluIleSerAsnAsnAspLysLeuGlnAspAspSerGluMetLeuProLysLysLeuLe 655
Db 4487 AGAGGATACCACTGGCTACCGGGCTCAGATAGACAAATCTCACCCGAGAAAACAGAGGCTT 4546
Qy 655 uLeuThrGluPheArgSerLeuValIleIysAsnSer-----ThrSerArgAsnPr 672
Db 4547 ATCTGAAGAAATAAGAGCGTG-----AAGAACACTTAACCCAGACACAGAGAATCT 4600
Qy 672 oSerGlyIleAsnAspTyrGlyGlnLeuLysAsnPheIysLysPheIysValTh 692
Db 4601 CAGGAGGTGGAGAGACATCCAAACAG-----CAAAGGCCAC 4639
Qy 692 rTyProGlyAlaGlyLysLeuProHisIleIleGlySerAspLeuIleAlaHisH1 712
Db 4640 T-----GGCTCTGAGGTG----- 4652

Qy 712 sAlaArgLysAsnThrGluLeuGluGluTrpLeuArgGln-----GluMetGluValG1 730
Db 4653 -TCTCAGAGGAAACAGCAGCTGGAGGTTGAGTGCAGACAAGTCACTCAGATGCCAACAGA 4711
Qy 730 nAsnGlnHisAlaLysGluGluSerLeuAlaAsp 741
Db 4712 GGAGAGCGTAAGATATAGCAATCTCTTGATGAT 4745

RESULT 8

US-09-606-421B-119
; Sequence 119, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangut, Chaitanya S.
; APPLICANT: Hoeken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Steiky, Yasar A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 119
; LENGTH: 8948
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-606-421B-119

Alignment Scores:
Pred. No.: 1.44e-06 Length: 8948
Score: 164.50 Matches: 187
Percent Similarity: 34.23% Conservative: 132
Best Local Similarity: 20.06% Mismatches: 295
Query Match: 4.22% Indels: 319
DB: 4 Gaps: 45

US-09-837-602-2 (1-754) x US-09-606-421B-119 (1-8948)

Qy 2 TrpLysLeuLeuProAlaAlaGlyProAlaGlyGluProTyrArgLeuLeuThrGly 21
Db 2331 TGGATGCTGATG-----GAGCTGCAGAAAGATTTCGAGGCAG 2366
Qy 22 ValGluTyrValValGlyArgLysAsnCysAlaIleLeuIleGluAsnAspGlnSerIle 41
Db 2367 ATAGACACTCGCGAGGCGAGGATGACTCTCAAAACCTCCCTCTAGCAGACCGGG--- 2423
Qy 42 SerArgAsnHisAlaValLeuThrAlaAsn-----PheSerValThrAsnLeuSerGln 59
Db 2424 TCCTTCACCACATCAGTCAAGTAAACGAGTAAAGAGTGTGCAGATGATTCACAA 2483
Qy 60 ThrAspGluIleProValLeuThrLeuLysAspAsnSerIysTyrGlyThrPheValasn 79
Db 2484 GCAATTCGTGAGGTTCTCAACAGCTTAAAGAT-----ATGCTTGCCAACTTCAGAGGT 2537
Qy 80 GluGluLys-----MetGlnAsn-----GlyPheSerArgThrLeuLysSer 93
Db 2538 TCTGAAAAGTACTGCTATTATTACAGAAATGAAGTATTTGGACTATTTCAGAAACTGGAAT 2597
Qy 94 GlyAspGlyIleThrPheGlyValPheGlySerLysPheArgIleGluTyrGluProleu 113
Db 2598 ATCAATGGTGTACAGATGGCTACTTAATAGCTTATGCACAGTAAG----- 2645
Qy 114 ValAlaCysSerSerCysLeuAspValSerGlyLysThrAlaLeuAsnGlnAlaIleLeu 133
Db 2646 -----GCACCTGCCAGGCTATTCTC 2666

[illegible]

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Qy 717 gGUuLeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLysGluGI 737
Db 2259 TGAATCTTCAGAAAGAACTAAATAAGAAAGTTGAA--GAAATGAAGCTTTGCGGAAGA 2315
Qy 737 u 737
Db 2316 A 2316

RESULT 10
US-09-220-132-79
; Sequence 79, Application US/09220132
; Patent NO. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shivjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 5857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-79

Alignment Scores:
Pred. NO.: 1.16e-06 Length: 5857
Score: 162.50 Matches: 101
Percent Similarity: 37.50% Conservative: 82
Best Local Similarity: 20.70% Mismatches: 176
Query Match: 4.17% Indels: 129
DB: 4 Gaps: 19

US-09-837-602-2 (1-754) x US-09-220-132-79 (1-5857)

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Qy 456 ArgAsnTyrPheGlnProSerThrLysLysArgGluArgAspGluGluAsnGlnGluMet 475
Db 3058 GAACAGACCCAGCAAGAGCTGCTTAAAGCATGAGGAAGAAAGATTCGAGAGG 3117
Qy 476 Ser---SerCysLysSerAlaArgIleGluThrSer-----CysSerLeuLeuGlu 491
Db 3118 AAATGTCGACCTGGAAAGAAATGGAACAACAGCCACCAACCACTGTCAGGAGCTGAAA 3177
Qy 492 GlnThrGlnProAlaThrProSerLeuTrpLysLysLysGluGlnHisLeuSerGluAsn 511
Db 3178 GCCAGGTATGAGAGCCACTTCTGAGACAAAACCAAGCATGAAGAAATCTCAGAGAAC 3237
Qy 512 GluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSerIle 531
Db 3238 -----CTCCAGAGACCGCTGTCGACACAGAGGACAAAGCTGAAGGCGCA 3282
Qy 532 ValLysAsnSerAlaSerLysSerHisAlaGluLysLeuArgSerAsnLysLysArg 551
Db 3283 CGGAGGAGAACAGTGGCTTCTGAGAGCTGAGGAGCTGAGAAAGCAAGCCGACAAA 3342
Qy 552 GluMetAspAspValAlaIleGluAsp-----GluValLeuGluGlnLeuPheLys--- 568
Db 3343 GCCAAGAGCTCTCAACAGCGGAGATGCCATGCAGATATGGAACAGATCACCAGAG 3402
Qy 569 -----AspThrLysProGluLeuGluLeuAspValLys 579
Db 3403 AAGACTGAGACTCTGGCCTCTTGGAGGACACCAAG-----CAACAAATGCAAAA 3453
Qy 580 ValGln-----LysGlnGluGluAspValAsn 588
Db 3454 CTACAGAAATGAATGGACACACTTAAAGAAACAACTTGAAGAAATGTGGAAGCTGAAC 3513
Qy 589 ValArgLysArgPro-----ArgMetAspIle 597
Db 3514 AAATCAAAAGAACTCTGACTGTAGAGAAATCAAAAATGGAAGATTTAGGAAGAATA 3573
Qy 598 GluThrAsnAspThrPheSerAspGluAlaValProGluSerSerLysLysGlnGlu 617
Db 3574 GAAACCCCTAAAGCAGGAGCAGCTCAGAAAGTCCAGCAGCTTTCAGCGGTTGCAAGAAG 3633
Qy 618 Asn-----GluIleGlyLysLysArgGluLeuLysGluAspSerLeuTrp 632
Db 3634 AACGTTAACTGCTGAGGAGCTGGGAGAGCAGGAGAC----- 3672
Qy 633 SerAlaLysGluIleSerAsnAspLysLeuGlnAspSerGluMetLeuProLys 652
Db 3673 -----GAAGTCACAGTCATCAAAAGCTGGAAGAGAAAGATCTGTCTCAATAAT 3723
Qy 653 LysLeuLeuLeuThrGluPheArgSerLeuValIleLysAsnSerThrSerArgAsnPro 672
Db 3724 CAGTTGTTA-----GAAATGAAAAAAGAGAAATCC 3753
Qy 673 SerGlyIleAsnAspAspTyrGlyGlnLeuLysAsnLysLysPheLysLysValThr 692
Db 3754 AAGTTCAATAAAGACGCAGATGAAGAGAAAGCTTCTTGCAGAAATCCATCAGTATAACT 3813
Qy 693 TyrProGlyAlaGlyLysLeuProHisIleIleGlyGlySerAspGluLeuAlaHis 712
Db 3814 -----ATGGCTTACTC----- 3825
Qy 713 AlaArgLysAsnThrGluLeuGluTrpLeuArgGlnGluMetGluVal---GlnAsn 731
Db 3826 ACAGAAAGGATCCGAGCTGGAGAAA---CTGAGAAATGAGGTACAGTCTCAGGGGA 3882
Qy 732 GlnHisAlaLysGluGluSerLeu 739
Db 3883 GAAACACGCTCTGCCAAGTCTCTG 3906

RESULT 11

US-09-107-532A-1575

; Sequence 1575, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1575:

SEQUENCE CHARACTERISTICS:
LENGTH: 3135 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...3135
SEQUENCE DESCRIPTION: SEQ ID NO: 1575:

US-09-107-532A-1575
Alignment Scores:
Pred. No.: 4.57e-07 Length: 3135
Score: 162.00 Matches: 172
Percent Similarity: 32.92% Conservative: 143
Best Local Similarity: 17.97% Mismatches: 293
Query Match: 4.15% Indels: 350
DB: 4 Gaps: 37

US-09-837-602-2 (1-754) x US-09-107-532A-1575 (1-3135)
Qy 51 AsnPheSerValThrAsnLeuSerGlnThrAspGluIleProValLeuLeuLysAsp 70
Db 168 AACTTCGGAAGACTTCGCTCTCGAAAGAGATGCGTCTTCTTGTCTACACCGACGA 227

Qy 71 AsnSerLysTyrGlyThrPheVal-----AsnGluLys 82
Db 228 AGAAACAAGCGTGACTTTTCTTTTGAACATCAGCAGATGAGCTATGAAATCGAACGAAA 287

Qy 83 MetGlnAsnGlyPheSerArgThr-----LeuLysSerGlyAsp-GlyI1 97
Db 288 ACCAGAACAAAGTTTACGAAAACGAAAGGAAACGGAACAAACAGGAGCCAAAGT 347

Qy 97 eThrPheGlyValPheGlySerLysPheArgIleGluTyrGluProLeuValAlaCysSe 117
Db 348 AACCTTGACCATTTTTCATGGAAAGGAAAA----- 378

Qy	117	rSerCysLeuAspValSerGlyLeuThrAlaLeuAsnGlnAlaIleLeuGlnLeuGlyG1	137
Db	379	-GAAATAAAACAATATCAAAACGATACAGACAGATCAGTTGATCAGAGAAGCTG-	432
Qy	137	yPheThrValAsnAsnTppThrGluGlyCysThrHisLeuVal	151
Db	433	---ATGAATCTCGATCGCAACACAGTTTCTCAAAATCGTTTACTACCCCAAGGAGA	485
Qy	152	---MetValSerValLysValThrIleLysThrIleCysAlaLeuLeuCy	167
Db	486	ATCCGTAATTTTTTGGTTTTCATCAAGCAGTCATATAAGAGAGACTGTTTACGTCATTTATT	545
Qy	167	sGlyArgProIleValLysProGluTyPheThrGluPheLeuLysAlaValGlnSerLy	187
Db	546	CGGTACTCAATTTTC---CHACAGTTCAATGAGCGATTAAAGAA---AAAGCAAA	596
Qy	187	sLysGlnProProGlnIleGluSerPhe-	196
Db	597	ACAACAGCA-ACAAAAATTGGATCATTTAGAGCAAGAGCTGCATCTTCTGCAAAAAGGT	655
Qy	197	-----	201
Db	656	TTGTTTGTAGTCAAAAGAGAACCCAGCAGCAGGTTTGAAGCGGTTTATAGCCCAATGGA	715
Qy	201	pGluProSerIleGlySerLysAsnValAspLeuSerGlyArgGlnGluArgLysGlnI1	221
Db	716	CAAAACATCA--GGCAATATCTCGAAAAACAATCACGGAAGAAAAAGAAAGCTCTAAAGG	772
Qy	221	ePheLysGlyLysThr-----PheIlePheLeuAsnAlaLysGlnHisLy	236
Db	773	AAC TTCAGAAAAACAAAGCAACTAGAAAAATTCCTACTATCGTTTCAAGAGCTTGAAA	832
Qy	236	sLysLeu-SerSerAlaValPheGlyGlyGlyGluAlaArgLeuIleThrGluGluA	256
Db	833	AAAGTTTATAGAAAAAAACGATATTAATAAACAGCAAAAGGAATTAGCTGTCAAAAAG	892
Qy	256	snGluGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAspThrGlyLeT	276
Db	893	ACGAAATAGAGAA-----	906
Qy	276	hrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIle-	290
Db	907	-----AAGAAACGATGGATGGGTATTATGAAATTA	937
Qy	291	--GlnSerIleMetAspMetLeuGlnArgGlnGlyLeuArgProIleProGluAlaGluI	310
Db	938	CGCAACGATTAGTCGAACCAATCCAGCGC-----CTACAGAAATAAAAGTTGAAAAA	991
Qy	310	leGlyLeuAla-----ValIlePheMetThrThrLysAsnT	322
Db	992	TAGAACTGTACAAAAAAGTAGTGAGCAACAAGAAACTAGCGATGACTACGCAGAAAT	1051
Qy	322	yrCysAspProGlnGlyHisProSerThrGlyLeuLysThrThrThrProGlyProSerL	342
Db	1052	ATGAAGAGTGGCAAAAAAATGAAGCAAAACCGGTACGCCGACAAACAAATAACAAAG	1111
Qy	342	euserGlnGlyValSerValAspGluLysLeuMetProSerAlaPro-	357
Db	1112	CTGCTCAAAACCTCAAAACAAACAGATGATGGTGCCAATTTGTGCAATCCTTACGTAGTA	1171
Qy	357	-----	357
Db	1172	AAAAACAAGCAGCGAACAATTAACAATTTTCATTGGATAAAGAAAGATTAAGATGCCGAGA	1231
Qy	358	-----ValAsnThrThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThrT	375
Db	1232	AGCTGTATCAAAATCTCGTATCTATCAGGAAGAAACTCGAAATTTCTCAAGAAAAATTAC	1291
Qy	375	rpAsp-----LeuSerG	379
Db	1292	TGGATCAGAAAAAACCTCAAGAAAGATCGTCTGCTTTTGGACACAGTTAAAAATATCTAGATG	1351

QY	379	luArgProLysGluIleLys-	-----ValSerLysMetG 390
Db	1352	AAAAAGCAGCAAGAATAATAGAAAAA	-----CGCTGGCTGCACAGATAA 1411
QY	390	luGlnLysPheArgMetLeuSerGlnAspAlaProThrVallYsGluSerCysLysThrs 410	
Db	1412	GAGAAAGACTCAAAAAGCACTGAAGAATAACA	-----TAGTCTATTGAAAGAAC 1471
QY	410	erSerAsnAsnAsnSerMetValSerAsnThrLeuAlaLysMetArgIleProAsnTyrg 430	
Db	1472	AGACAGACAAGCAGAGACAGCTGAAAGCCAATGGCGCAAAGCAAAATGGCTCGTCCTTC 1531	
QY	430	lnLeu-	-----S 432
Db	1532	AGCTTTTTCGCTCCAGGGGAGCCATGTCTTGTTGTGGATCAACGGAAACACCCTCATC 1591	
QY	432	erProThrLysLeuProSerIleAsnLysSerLysAspArgAlaserGlnGlnGln- 450	
Db	1592	AACAATTAACACCAAGCAGCAAAATGAAGATATCTTTAAAGTAGAACAACAACCTGG 1651	
QY	451	--GlnThrAsnSerIleArgAsnTy-PheGlnProSerThrLysLysArgGluArgAspG 470	
Db	1652	CAGAAGCTGAGTCTGCTGTAGAAGAACTCAGCAAAATCAITGCCAAAGTGAAGCACATG 1711	
QY	470	luGluAsn----	GlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCys 488
Db	1712	AAAATATCTTCAACAACAAATATCAGATTAGAACAAAAATCATGGCAACGAATATAC 1771	
QY	488	erLeuLeuGluGlnThrGln-	-----ProAlaThrProSerLeut 501
Db	1772	AATTGGCTTGAAACAGAGAACACTTGCAACAGGCTTTGAAAGGCAATTTCTCTGAGATAA 1831	
QY	501	rLysAsnLys-	----- 504
Db	1832	CAGAACAAAAACAAAAACAACCTCTTGTTAGTAATCGAACAAUCTTTAGATAGACGAAAAA 1891	
QY	505	-----	-----G 505
Db	1892	GCAAGATGGCCAATGCAAGAATAAGAGCTGGAAGAAATAAGACAACAAGCAGAAAAAGCTCG 1951	
QY	505	luGlnHisLysSerGluAsnGluProValAspThrAsnSerAspAsnAsnLeu--PheT 524	
Db	1952	AACCAAAITAGCTGTCTACAAACAGCAGCAGACAGAAAAATAATACGCTCCAGCAAC 2011	
QY	524	hrAspThrAspLeuLysSerIle-----	VallYsAsnSerAlaSerLysSerHisa 541
Db	2012	TGCAAGGAGAAATCAAAAGTTTAGAACACAATTCGAGATACGGATAGTAAGCTGTTAG 2071	
QY	541	laalaGluLysLeuArgSerAsnLysArgGluMetAsp-----	AspValAlaIleg 559
Db	2072	AAGAGGAGATACGACACTTGAAAAACAGTTAGAAGAGACTCGAATCAACTAGCTGTTG 2131	
QY	559	luAspGluValLeuGluGlnLeuPheLysAsp-	-----ThrLysProGluL 574
Db	2132	AGCAGAAAGCAGAGTGCAATGTTTCGAGATCTTCATACGCTTCGACACAGACTTGATC 2191	
QY	574	eUGlu-----	IleAspValLysValGlnLysGlnGluAspVala 588
Db	2192	TTCAACATGAACAAATAGAAAAAATAGATCAAAAAATAGAAAAAGGAAACAAAGAAAGATAG 2251	
QY	588	snVal-----	----- 589
Db	2252	CTAAAAAGTTAGAAAGCCAGTCGTATTTTTTCAACAATCGAAGAAATCTGTGCAATTGGCAC 2311	
QY	589	-----	----- 589
Db	2312	AACAGCAAGCACAATATAAAGAAAAACCAAGTACAGTTACTTCTTATCATGAAGCAANT 2371	
QY	590	-----	ArgLysArgProArgMetAspIleGluThrAsnAspThrPheSerA 605
Db	2372	TAGTGACAGCTGACCGGCTGCGCTCAATTAGAAAAATATCCAGCTAACTGAGACATTC- 2427	
QY	605	spGluAlaValProGluSerSerLysIleSerGlnGlu--	AsnGluIleGluLVaLVsa 624

Db 2428 -----CNGATACAGAGATACCCACAGTTAGAGAAATAGACGTATGA 2476
Qy 624 rgGluLeuLysGluAspSerLeuTrpSerAlaLysGluLeuSer---AsnAsnAspLysL 643
Db 2477 TCGAATAAAGCAAGAAAGATATACGGTTTACAGAGACAAATAATAGTAAATCAAAAA 2536
Qy 643 euGlnAspAspSerGluMetLeuProLysLysLeuLeuLeuThrGluPheArgSerLeuV 663
Db 2537 TCTACGAT-----GAATGCTTTTCGATTT 2560
Qy 663 alileLysAsnSerThrSerArgAsnProSerGlyLleAsnAspAspTyrGlyGlnLeuL 683
Db 2561 ATCACACACAGCACCAATTA-----GATGAGCTTACGCAATAC 2602
Qy 683 ysnPheLysPheLysValThrTyrProGlyAlaGlyLysLeuProHisileI 703
Db 2603 AGCAGCTTTCGCA-----ACATTCAACGAGAGAAATCCT----- 2637
Qy 703 leGlyGlySerAspLeuLeAlaHisAlaArgLysAsnThrGluLeuGlu----- 721
Db 2638 -----AAGAAGACTAGTTTGGACGGTATG 2662
Qy 722 -----TrpLeuArgGlnGluMetGluValGlnAsnGlnHisAlaLys----- 735
Db 2663 TGCTTCAGGTTTATCTTCAAGAGTGTACAGTAGCAATGATCATCTCCAAGCTTTAA 2722
Qy 736 -----GluGluSerLeuAlaAspLeuPheArgTyr 746
Db 2723 CGAAAAATCGTTATCAATTTGAGCTAGCGGATACCATTCGCAGTTAT 2769

RESULT 12

US-08-923-992A-7
Sequence 7, Application US/08923992A
Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IGA Fc Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/923, 992A
APPLICATION NUMBER: US/08-923, 992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3294 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3294
US-08-923-992A-7
Alignment Scores:
Pred. No.: 6,39e-07 Length: 3294
Score: 161.00 Matches: 141
Percent Similarity: 37.11% Conservative: 124
Best Local Similarity: 19.75% Mismatches: 233
Query Match: 4.13% Indels: 216
DB: 3 Gaps: 39
US-09-837-602-2 (1-754) x US-08-923-992A-7 (1-3294)
Qy 192 GlnleGluSerPheTyrProLeuAspGluProSerileGlySerLysAsnValasp 211
Db 298 CAGAAAATGAGTTTAAACAAAATTTGATGAACAATGATCTGATGATTATTAGAA 357
Qy 212 LeuSerGlyArg-----GlnGluArgLysGlnIle 221
Db 358 TTAGAAAATCAATTTAAACGAACTAATAGACTGTTACACATCAACACATGAAGAAGTT 417
Qy 222 PheLysGlyLysThrPheLlePheLeuAsnAlaLysGlnHisLysLysLeuSerSerAla 241
Db 418 GAGAAAGATAAG-----AAAGCTTAAGCAACAGAAAACTCTGAAACACATCA 462
Qy 242 ValValPheGlyGlyGluAlaArgLeuIleThrGluLysGlnGluGluHisAsn 261
Db 463 -----GATACGAAAGTAGATCTTAAGCAATATTGACAAAGAGCTTTAAT 504
Qy 262 PhePheLeuAlaProGlyThrCysValValAspThrGlyIleThrAsnSerGlnThrLeu 281
Db 505 CATCAAAAAGTCAA-----GAAGCGGATCAACAAATGAAGAT----- 543
Qy 282 IleProAspCysGlnLysLysTrpIleGlnSerIleMetAspMetLeuGlnArgGlnGly 301
Db 544 ---AAAGATTCTATGCTGAAAAATTCGAAGATATTTCGTAACAAAGCTCAACACAGAT 600
Qy 302 LeuArgProileProGluAlaGluIle-----GlyLeuAlaValIlePheMetThrThr 319
Db 601 AAAAAAGAGATCCGAAAGTAAAGTTTCGTAAGAACTAGGTAAACTCTTTAGTTCAACT 660
Qy 320 LysAsnTyrCysAspPro-----GlnGlyHisProSerThrGlyLeuLysThrThr 337
Db 661 AAAGCTGGTCTGATCAAGAAATTCAGACCAT-----GTGAAGAAAGAAACG 708
Qy 338 ProGlyProSerLeuSerGlnGlyValSerValAspGluLysLeuMetProSerAlaPro 357
Db 709 AGTAGTGAGGAAAATACTCAG-----AAAGTTGATGAACACTAT----- 747
Qy 358 ValAsnThrThrThrValAlaAspThrGluSerGluGlnAlaAspThrTrpAspLeu 377
Db 748 GCTAATAGCTTTCAGAACCTTGCTCAAAAATCTCTTGAAGAACTAGATAGGCAACTACC 807
Qy 378 SerGluArgProLysGluIleLysValSerLysMetGlu-----GlnLys----- 392
Db 808 ATGAACAAGCTACACAAGTTAAAAATCAATCTTTAGAAAACGCTCAAAAGCTCAAGAA 867
Qy 393 -----PheArgMetLeuSerGlnAspAla 400
Db 868 ATCAACCTCTTATCAAGAAACGAATGTGAAATTTGATAAGGCTATGAGTGAGAGCTTG 927
Qy 401 ProThrValLysGluSerCysLysThrSerSerAsnAsn-----SerMetValSer 418
Db 928 GAGCAGGTTGAGAAGGAATTTAAACATAATTCGGAAGCTAATTTAGAAAGATTTGGTTGCG 987
Qy 419 AsnThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLys-----LeuPro 437
Db 988 AAATCTAAAGAAATCTGTAAGAGAAATACGAAGGAAAACTTAATCAATCTAAATACTTCCA 1047
Qy 438 SerIleAsnLysSerLysAspAlaSerGln-----GlnGlnGlnThrAsnSerIle 455

Db 1666 GAGTCCGAAGAAGATGACTCAGAGAAAGAGCTGTGATGAAGACTGCTCTGTAAGAACAGCTCT 1725
Qy 452 ThrAsnSerIleArgAenTyPheGlnProSerThrLysLysArgGluAArgAspGluGlu 471
Db 1726 GAAGATGGCTCCGAGAGAGATTTTGAAGAAATGGCTCGAGAAAGATTTTGGACAGAGAA 1785
Qy 472 AsnGlnGluMetSerSerCysLysSerAlaAArgIleGluThrSerCysSerLeuLeuGlu 491
Db 1786 GGTCTTGAA----- 1794
Qy 492 GlnThrGlnProAlaThrProSerLeuTrrpLysAsnLysGluGlnHisLeuSerGluAsn 511
Db 1795 -----MAGGAGCTTCATGAAATGTTCTTGACAAA 1824
Qy 512 GluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSerIle 531
Db 1825 GAGTTAGAGAAATGACTCTGAAATCTCGAATTTGAAGATGACGGCTCTGAAAGATG 1884
Qy 532 ValLysAsnSerAlaBerLysSerHisAlaAlaGluLysLeuArgSerAsnLysLysArg 551
Db 1885 TTAGATGAGGAAGGCTCTGAGAGAGAGATTTGACGAAGAT-----TCAGATGAAAGAGAA 1938
Qy 552 GluMetAspAspValAlaIleGluAspGluValLeuGluGlnLeuPheLysAspThrLys 571
Db 1939 GAA-----GAGGAGGATACATATGAAAGATATTGTGATGATGACTCT 1980
Qy 572 ProGluLeuGluIleAspValLysGlnGlnLysGlnGluAspValAsnValArgLys 591
Db 1981 GATGAGAAAGAG-----GATGAGAGATATGCAGATGAAAGGGG 2019
Qy 592 ArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaVal----ProGlu 610
Db 2020 CTTGAAGCTCTGATAAAAGGCGGAAGGTGATGCAGATGAAAGCTGTTTGAAGAG 2079
Qy 611 SerSerLysIleSerGlnGluAsnGluIleGlyLysLysArgGluLeuLysGluAspSer 630
Db 2080 TCAGATGACAAAGAAAGATGAAGATGCAGATGCGAAGGAAGTTCGAAGATGCTGACGAAAG 2139
Qy 631 LeuTrpSerAlaLysGluIleSerAsnAsnAspLysLeuGlnAspAspSerGluMetLeu 650
Db 2140 TTGTTC-----GAAGATGATGATTCCTCAATGAGAAGTTGTTGATGAGGAGGAAGATTC 2193
Qy 651 ProlLysLysLeuLeuLeuThrGluPheArgSerLeuValIleLysAsnSerThrSerArg 670
Db 2194 AGTGAGAAGTTGTT----- 2208
Qy 671 AsnProSerGlyIleAsnAspAspTyrGlyGlnLeuLysAsnPhelLysLys-PhelLys 690
Db 2209 -----GACGATTCTGATGAGGGGACATTGGGTGTTTGGGAGTGTGGAAGAA 2259
Qy 690 svalThrTyrProGlyAlaGlyLysLeu 699
Db 2260 GGGCCCTATCCACTGCGACAGCTTTA 2287

RESULT 14
US-09-214-564A-1
; Sequence 1, Application US/09214564A
; Patent No. 6150515
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Zhou, Qiang
; TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
; TITLE OF INVENTION: Elongation By HIV-1 TAT
; FILE REFERENCE: M0656/7042
; CURRENT APPLICATION NUMBER: US/09/214,564A
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/021,218
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/033,152
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/US97/11713
; PRIOR FILING DATE: 1997-07-03

REF ID: A66091
HIS-09-214

; Patent No. 6150515

; APPLICANT: Sharp, Phillip A.

; TITLE OF INVENTION: TAT-SF: Cofactor Fo

; FILE REFERENCE: M0656/7042

; CURRENT FILING DATE: 1999-08-18

;
PRIOR FILING DATE: 1996-07-03

;; PRIOR FILING DATE: 1996-12-13

1997-07-03

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..2371
; NAME/KEY: unsure
; LOCATION: 46..46
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: unsure
; LOCATION: 2731..2731
; OTHER INFORMATION: n = a, c, g or t
; US-09-214-564A-1

Alignment Scores:
Pred. No.: 1.18e-06 Length: 2815
Score: 157.50 Matches: 138
Percent Similarity: 31.92% Conservative: 95
Best Local Similarity: 18.90% Mismatches: 259
Query Match: 4.04% Indels: 238
DB: 3 Gaps: 29

US-09-837-602-2 (1-754) x US-09-214-564A-1 (1-2815)

Qy 59 GlnThrAspGluLeuProValLeuThrLeuLysAspSerLysTyGlyThr----- 76
Db 599 CAGACAGAGAAATTTAAGGCTAAACTTTTACAAAGATATCAAA-----GGAAATCTTAAA 652
Qy 77 -----PheValAsnGluLysMetGlnAsnGlyPheSerArgThr 90
Db 653 GGACAGCGTCTTCTGTTATTTGAAAGAGAAATCTGTGNA-----CTTGCA 700
Qy 91 LeuLysSerGlyAsp-----GlyLeuThrPheGlyValPheGlySerLys 105
Db 701 TTAATACTTTTGGATGAAGATGAAATTTAGAGGCTACAAATTTACATGTTGAGGTGGCAAG 760
Qy 106 PheArgLeu-----GluTyrGluProLeuValAlaCysSerSerCysLeuAspValSer 123
Db 761 TTTCAACTGAAGGAGAGATATGATGCTCTCAAGAGAGAGAGAGAGATATTAAG 820
Qy 124 GlyLysThrAlaLeuAsnGlnAlaLeuGlnLeuGlyGlyPheThrValAsnAsnTyr 143
Db 821 AAGAGCTGTCTATGCAACAAAGCAGTTG-----GATTGG 856
Qy 144 ThrGluGlu-----CysThrHis----- 149
Db 857 AGACCTGAGAGCGCGGACCATCCCGGATGCGCCATGAGCGAGTTGTTCATCATCAAG 916
Qy 150 -----LeuValMetValSerValLysVal 157
Db 917 AATATGTTTCATCCTATGATTTTGGAGATGATCCGTTGGTGGTGAATGATGAGAGAA 976
Qy 158 ThrIleLysThrIleCysAlaLeuIleCysGlyArgProIleValLysProGluTyrPhe 177
Db 977 GACCTTCGAGTAGAGTGTG-----AAGTTT 1003
Qy 178 ThrGluPheLeuLysAlaValGlnSerLysLysGlnProGlnIleGlu-----Ser 195
Db 1004 GGACAAATTAGGAAACTCTTCTCTTTGATAGGACCCAGATGTTGGTGGCTCTGTGTCC 1063
Qy 196 PheTyrProProLeuAspGluProSerIleGlySerLysAsnValAsp-----Leu 212
Db 1064 TTTGGGATCCA---GAGGAGCTGATGATTTGTTATTCAGACTCTCGATGGAGATGGTTT 1120
Qy 213 SerGlyArgGlnGluArgLysGlnIlePheLysGlyLysThrPheIlePheLeuAsnAla 232
Db 1121 GGTGGCCGTCAATCACTGCGGAGGATGGATGGGACTACA----- 1162
Qy 233 LysGlnHisLysLysLeuSerSerAlaValValPheGlyGlyGlyGluAlaArgLeuIle 252
Db -----
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1163 -----GATTATCAGGTGGAGGAAACC 1183
253 ThrGluGluAsnGluGluHisAsnPhePheLeuAlaProGlyThrCysValValAsp 272
1184 TCAAGAGAAAGGAGGAAAGG----- 1204
273 ThrGlyIleThrAsnSerGlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSer 292
1205 -----CTGAGAGGATGG----- 1216
293 IleMetAspMetLeuGlnArgGlnGlyLeuArgProIleProGluAlaGluIleGlyLeu 312
1217 -----GAGGCTTTCTCAATGCTCTGAGGCCAACAGAGGCGCTT 1255
313 AlaValIlePheMetThrThrLysAsnTyrCysAspPro-----Gln 326
1256 AGCGTTCAAGATTCGTCTCTGCTTCGAAAGGCGAGGCGCTTCTAGAGCAAGGCATTTTCA 1315
327 GlyHisProSerThrGly----- 332
1316 GAGCACCCCGACACATCTAAATGAATGCTCAAGAAACTGCAACTTGAATGGCATTTGAA 1375
333 -----LeuLysThrThrThrProGlyProSerLeuSerGlnGly 345
1376 GAACCTATAGATGAGAAGAGAGTTTGAAGACACAGAGATGGGGAGAAATTTGAAGAGGT 1435
346 ValSerValAspGluLysLeuMetProSerAlaProValAsnThrThrThrTyValAla 365
1436 GCTTCTGAAACAACTCTAAGGAAAGTAGCCCGGAAAGAGAGCTGAAGAGGCTGCCT 1495
366 AspThrGluSerGluGlnAlaAspThrTrpAspLeuSerGluArgProLysGluIleLys 385
1496 GAAAGAGATCTCAAGAGGC-----TGCCCCAAAGAGGGTTTGAAGGCGAGC 1543
386 ValSerLysMetGluGlnLys-----PheArgMetLeuSerGlnAspAlaPro 401
1544 TGCTCCCAAAAGAGCTGGAAGAGCAATCCCGTAAAGAGAGCTGGAAGAGGATAGTCT 1603
402 ThrValLysGluSerCysLysThrSerSerAsnAsnSerMetValSerAsnThrLeu 421
1604 -----AAAAAGAGCTTAAAGAGACACACTCAAAATGATTTGTGAGAGATGGCCTT 1657
422 AlaLys-----MetArgIleProAsnTyrGlnLeuSerProThrLys 435
1658 GCAAGAGAACTCTGAGATGACCTCAACAAGAGGCTCTGAAGAGGAGGTGGCCCCACAAA 1717
436 Leu-----ProSerIleAsnLysSerLysAspArgAlaSerGlnGlnGln 451
1718 GAGTCCGAGAGAGATGACTCAGAGAAAGAGTCTGATGAAGACTGCTCGAAAAACAGTCT 1777
452 ThrAsnSerIleArgAsnTyrPheGlnProSerThrLysLysArgGluArgAspGluGlu 471
1778 GAAGATGGCTCCGAAAGAGAAATTTGAAGAAATGGTCTCGAGAAAGATTTGGACGAGAA 1837
472 AsnGlnGluMetSerSerCysLysSerAlaArgIleGluThrSerCysSerLeuLeuGlu 491
1838 GGTCTCTGAA----- 1846
492 GlnThrGlnProAlaThrProSerLeuTrpLysAsnLysGluGlnHisLeuSerGluAsn 511
1847 -----AAGAGCTTCATGAAATGTTCTTGACAAA 1876
512 GluProValAspThrAsnSerAspAsnAsnLeuPheThrAspThrAspLeuLysSerIle 531
1877 GAGTTAGAGAAATGACTCTGAAACTCCGAATCCGAATGACGCTCTGAAAAAGTG 1936
532 ValLysAsnSerAlaSerLysSerHisAlaAlaGluLysLeuArgSerAsnLysArg 551
1937 TTAGATGAGGAGCGCTCTGAGAGAGAGTTTGAACAGAT-----TCAGATGAAAGGAA 1990
552 GluMetAspValAlaIleGluAspGluValLeuGlnLeuPheLysAspThrLys 571
1991 GAA-----GAGGAGGATACATATGAAAGATTTTGTATGATGAGTCT 2032
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Qy 572 ProGluLeuGluLeuAspValIysValGlnIysGlnGluAspValAsnValArgIys 591
Db 2033 GATGAGAAAGAG-----GATGAAGAATATGCAGATGAAGAAGGG 2071

Qy 592 ArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaVal--ProGlu 610
Db 2072 CTTGAGCTGCTGATAAACGCGGAAGAGGTGATGCAGATGAAGAAGCTTTTGAAGAG 2131

Qy 611 SerSerIysIleSerGlnGluAsnGluIleGlyIysIysArgGluLeuLysGluAspSer 630
Db 2132 TCAGATCAAGGAAGATGAAGATGCAGATGGAAGGAAGTTGAAGATGTCGACGAAAG 2191

Qy 631 LeuTrpSerAlaLysGluIleSerAsnAsnAspIysLeuGlnAspSerGluMetLeu 650
Db 2192 TTGTTC-----GAAGATGATGATTCCAATGAGAAGTTGTTTGTATGAGGAGGAAGATTCC 2245

Qy 651 ProLysIysLeuLeuLeuThrGluPheArgSerLeuValIleLysAsnSerThrSerArg 670
Db 2246 AGTGAGAAGTTGTT----- 2260

Qy 671 AsnProSerGlyIleAsnAspAspIysGlyGlnLeuLysAsnPheLysLys-PheLysLY 690
Db 2261 -----GACGATTCGTGAGAGGGGACTTTGGTGGTTTGGGAGTGTGAAGAA 2311

Qy 690 sValThrTyrProGlyAlaGlyLysLeu 699
Db 2312 GGGCCCTATCCACTGCGCAGCAGCTTTA 2339

RESULT 15
US-08-242-932-1
; Sequence 1, Application US/08242932
; Patent No. 5595740
; GENERAL INFORMATION:
; APPLICANT: Brady, L. Jeannine
; TITLE OF INVENTION: Cloning of No. 5595740-IgA Fc Binding Forms of
; TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/242,932
; FILING DATE: 16-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-242-932-1

Alignment Scores:
Pred. No.: 2.63e-06 Length: 4200
Score: 157.00 Matches: 144

Percent Similarity: 36.96% Conservative: 121
Best Local Similarity: 20.08% Mismatches: 236
Query Match: 4.03% Indels: 216
DB: 1 Gaps: 40

US-09-837-602-2 (1-754) x US-08-242-932-1 (1-4200)

Qy 192 GlnIleGluSerPheTyrProProLeuAspGluProSerIleGlySerLysAsnValAsp 211
Db 710 CAGAAAAATGAGTTTAAAAACAAAAATGATGAAACAAATGATTCGTGATGATTAGAA 769

Qy 212 LeuSerGlyArg-----GlnGluArgLysGlnIle 221
Db 770 TTAGAAAAATCAATTTAACGAAACTTAATPAGACTGTTCACACATCAACAAACATGAAGAAGTT 829

Qy 222 PheLysGlyIysThrPheIlePheLeuAsnAlaLysGlnIleLysLysLeuSerSerAla 241
Db 830 GAGAAAGATAG-----AAAGCTTAAGCAACAGAAAAACTCTGAAACAGTCA 874

Qy 242 -----ValValPheGlyGlyGluAlaArgLeuIleThrGluGluAsnGluGlu 258
Db 875 GATACGAAAGTAGATCTAAGCAATATTGACAAAGAGCTTAATCATCATCAAAAAAGTCAAGTT 934

Qy 259 GluHisAsnPhePheLeuAlaProGlyThrCysValValAspThrGlyIleThrAsnSer 278
Db 935 GAA-----AAAATGCGAGAGCAAAAGGCAATCACAATGAA 970

Qy 279 GlnThrLeuIleProAspCysGlnLysLysTrpIleGlnSerIleMetAspMetLeuGln 298
Db 971 GAT-----AAAGATTCTATGCTGAAAAAATCGAAGATATTCTGTAACAAAGCTCAA 1021

Qy 299 ArgGlnGlyLeuArgProIleProGluAlaGluIle-----GlyLeuAlaValIlePhe 316
Db 1022 CAACGAGATAAAAAAGAGATGCCGAAGTAAGGTTGCTGAAGAACTAGGTAACTCTTT 1081

Qy 317 MetThrThrLysAsnTyrCysAspPro-----GlnGlyHisProSerThrGlyLeuLys 334
Db 1082 AGTTCAACTAAAGCTGCTGATCAAGAAATTCAGAGCAT-----GTCAAG 1129

Qy 335 ThrThrThrProGlyProSerLeuSerGlnGlyValSerValAspGluLysLeuMetPro 354
Db 1130 AAAGAAACGAGTAGTAGGAAAAATACTCAG-----AAAGTTGATGAACACTAT- 1177

Qy 355 SerAlaProValAsnThrThrTyrValAlaAspThrGluSerGluGlnAlaAspThr 374
Db 1178 -----GCTAATAGCCTTCAGACCTTGCTCAAAAATCTCTTGAAGAACTAGATAAG 1228

Qy 375 TrpAspLeuSerGluArgProLysGluIleLysValSerLysMetGlu-----GlnLys 392
Db 1229 GCAACTACCAATGAACAAGCTACACAAGTTAAAAATCAATTCCTAGAAAAACGCTCAAAAG 1288

Qy 393 -----PheArgMetLeuSer 397
Db 1289 CTCAAAGAAATACAACCTCTTATCAAAAGAAACGAATGTGAATTTGTAAGGCTATGAT 1348

Qy 398 GlnAspAlaProThrValLysGluSerCysLysThrSerSerAsnAsnAsn-----Ser 415
Db 1349 GAGAGCTTGAGCAGGTTGAGAGGAATTAACAATAATTCGGAAGCTAATTTAGAAGAT 1408

Qy 416 MetValSerAsnThrLeuAlaLysMetArgIleProAsnTyrGlnLeuSerProThrLys 435
Db 1409 TTGTTGCGAAATCTAAAGAAATCGTAAGAGATACGAAGGAAACAACTTAATCAATCTAAA 1468

Qy 436 ----LeuProSerIleAsnLysSerLysAspArgAlaSerGln-----GlnGlnGlnThr 452
Db 1469 AATCTTCCAGATTTAAAGCAACTAGAGAGGAAGCTCATTCGAAGTTGAAACAAAGTTGTG 1528

Qy 453 AsnSerIleArgAsnTyrPhe-----GlnProSerThrLysLysArg-----Glu 467
Db 1529 GAGGATTTTGAAGAAAAATTTAAACGCTCAGACAGTGCAGACCAAAAAACGCTGTCAA 1588

Qy 468 ArgAsp-----GluGluAsnGlnGluMetSerSerCysLysSerAlaArgIle 483
Db 483 -----GluGluAsnGlnGluMetSerSerCysLysSerAlaArgIle 483

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Db 1589 CGAGATTAGCTGCTAATAAGAAATAATCAACAA-----AGATT 1627
Qy 484 GluThrSerCysSerLeuLeuGluGlnThrGlnProAlaThrProSerLeuTrpLysAsn 503
Db 1628 GAGTTAACAGTTTCA-----CCAGAGATATCACTGTATATGAAGGT 1669
Qy 504 LysGluGlnHisLeuSerGluAsnGluProValAspThrAsnSerAspAsnAsnLeuPhe 523
Db 1670 GAAGACGTGAATAATTACA-----GTCACAGCTAAAGCTGATTCGAAGACGACG 1717
Qy 524 ThrAsp---ThrAspLeuLysSerIleValLysAsnSerAlaSerLysSerHisAlaAla 542
Db 1718 TTGCACTTCAGTGATCTT-----TTAACAAATATATATCCGTCGTATCA----- 1762
Qy 543 GluLysLeuArgSerAsnLysLysArgGluMetAspValAlaIleGluAspGluVal 562
Db 1763 GATAGAATTAGTACAAATTATAGACTAACACGGATTAATCATAGATTGCCGAAATCACT 1822
Qy 563 LeuGluGlnLeu-----PheLysAspThrLys 571
Db 1823 ATCAAGAATTGTGAAGCTAAATGAAAGTCAACACAGTGACTCTAAAGGCTAAAGATGATTCT 1882
Qy 572 -----ProGluLeuGluIleAspValLysValGlnLysGlnGluAspValAsn 588
Db 1883 GGCAATGTAGTTGAAATAAACATTCACTATTACAGTCAAAAGAAAGAGGAGAA---CAA 1939
Qy 589 ValArgLysArgProArgMetAspIleGluThrAsnAspThrPheSerAspGluAlaVal 608
Db 1940 GTTCTTAACACCA-----GAGCAGAAAGATTCTAAACCGGAAGAAAGGTT 1987
Qy 609 ProGluSerSerLysIleSerGlnGluAsnGluIle-----GlyLysLys 623
Db 1988 CCTCAAGAACCAAAATCAAAATGACAAGATCAATTACAAGAGTTGATTAAATCAGCTCAA 2047
Qy 624 ArgGluLeuLys----- 627
Db 2048 CAAGAAGCTGGAAAGATTAGAAAAAGCAATAAAGAAATTAATGGAGCAACACGAGATTCCA 2107
Qy 628 -----GluAspSerLeuTrp---SerAlaLysGlu----- 636
Db 2108 TCCAAATCCAGAGATATGTTTCAAAATCTATTGCGAGTCACAAAAGAGCCTATCCAG 2167
Qy 637 -----IleSerAsnAsnAspLysLeuGlnAspAspSer----- 647
Db 2168 GAAGCCATAACAAGTTTAAAGATATTGTTGATTCATCTTCAAAATACTACACAGAG 2227
Qy 648 -----Glu 648
Db 2228 CACTATTTAACAAATAATAATCTGATTTTATGAATTATCAACTTCATGCACAAATGGAG 2287
Qy 649 MetLeuProLysLysLeuLeu-----ThrGluPheArg 660
Db 2288 ATGCTGACTAGAAAGTGTTTCAGTATATGAAACAAATATCCTGATATGCGAAATTAAT 2347
Qy 661 SerLeuValIleLysAsnSerThrSerArgAsnProSerGlyIleAsnAspAspTyrGly 680
Db 2348 AAG---ATATTTGAGTCAGATATGAAGAGACGAAA-----GAAGATAATTACGGA 2395
Qy 681 GlnLeuLysAsn-----PheLysLysPhe----- 688
Db 2396 AGTTTAGAAATATGATGCTTTGAAAGGCTATTTTGAAGAAATATTCCTTACACCATTTAAT 2455
Qy 689 -----LysLysValThrTyrProGlyAlaGlyLys 698
Db 2456 AAAATTAAAGAGATTGTAGATTGTTGGATAAAAAAGTAGAACAGATCAGCCAGCACCA 2515
Qy 699 LeuProHisIleIleGlyGlySerAspLeuIleAlaHisHisAlaArgLysAsnThrGlu 718
Db 2516 ATTCGGAA-----AATTCAGAAATGATCAGGCTAAGGAAAGGCTAAGATTGCT 2566
Qy 719 LeuGluGluTrpLeuArgGlnGluMetGluValGlnAsnGlnHis-----AlaLysGlu 736
Db 2567 GTATCGAAGATATAGTAGAGGTTTATGATGGAGTTTCAACATCTGCAGAGAAAAAAT 2626
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Qy 737 GluSerLeuAlaAspAspLeuPheArgTyrAsnProTyrLeuLysArgArg 753
Db 2627 AACAGTAAAAATTGTTGATCTTTTAAAGGAACTTGAAGCGATTAAACAACAA 2677
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Search completed: January 6, 2004, 14:55:53
Job time : 220 secs

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OM nucleic - nucleic search, using sw model

Run on: January 6, 2004, 10:38:54 ; Search time 1312 Seconds
(without alignments)
11615.852 Million cell updates/sec

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Perfect score: 4403
Sequence: 1 ttccgacagggcgcgggtg.....accgcggtagctccagct 4403

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2263443 seqs, 1730637950 residues

Total number of hits satisfying chosen parameters: 4526886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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- 13: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	552.2	12.5	646	10	US-09-833-263-343
C 3	552.2	12.5	646	14	US-10-025-380-343
4	537.4	12.2	541	10	US-09-878-178-1737
5	537.4	12.2	541	14	US-10-046-935-1737
6	537.4	12.2	541	15	US-10-146-502-1737
7	507	11.5	587	15	US-10-102-524-532
8	405.6	9.2	468	11	US-09-918-995-13834
9	258.4	5.9	360	10	US-09-783-590-3449
10	239.4	5.4	272	9	US-09-923-876-5167
11	239.4	5.4	272	12	US-09-923-876-5167
C 12	212.6	4.8	475	10	US-09-917-800A-803
13	191	4.3	404	10	US-09-783-590-8929
14	167.6	3.8	315	10	US-09-960-352-8727
15	119.4	2.7	442	9	US-09-864-761-11287

16	114	2.6	114	9	US-09-864-761-27987	Sequence 27987, A
17	97.6	2.2	6237	13	US-10-311-455-331	Sequence 331, App
C 18	92.4	2.1	6237	13	US-10-311-455-332	Sequence 332, App
C 19	73.6	1.7	539	15	US-10-198-846-1369	Sequence 1369, Ap
20	72	1.6	9539	13	US-10-240-453-54	Sequence 54, Appl
21	72	1.6	9539	15	US-10-239-676-52	Sequence 52, Appl
C 22	71	1.6	14006	13	US-10-311-455-1931	Sequence 1931, Ap
C 23	70	1.6	6056	13	US-10-311-455-753	Sequence 753, App
24	69.6	1.6	15548	13	US-10-311-455-2128	Sequence 2128, Ap
25	69.6	1.6	3673778	13	US-10-312-841-1	Sequence 1, Appl1
26	69.6	1.6	3673778	13	US-10-312-841-2	Sequence 2, Appl1
C 27	69.2	1.6	2787	11	US-09-764-891-8349	Sequence 8349, Ap
C 28	69.2	1.6	2787	15	US-10-205-428-782	Sequence 782, App
29	68.2	1.5	6171	13	US-10-311-455-761	Sequence 761, App
30	68.2	1.5	6668	13	US-10-311-455-1670	Sequence 1670, Ap
31	68.2	1.5	8392	13	US-10-311-455-1463	Sequence 1463, Ap
32	67.2	1.5	446	10	US-09-960-352-3400	Sequence 3400, Ap
33	67	1.5	6145	13	US-10-311-455-945	Sequence 945, App
34	66.8	1.5	27007	10	US-09-764-868-1424	Sequence 1424, Ap
35	66.6	1.5	529	10	US-09-983-965-2109	Sequence 2109, Ap
36	66.2	1.5	17594	13	US-10-311-455-1999	Sequence 1999, Ap
37	65.8	1.5	6631	13	US-10-240-453-214	Sequence 214, App
C 38	65.8	1.5	6668	13	US-10-311-455-1670	Sequence 1670, Ap
39	65.2	1.5	6668	13	US-10-311-455-1669	Sequence 1669, Ap
C 40	65	1.5	8392	13	US-10-311-455-1463	Sequence 1463, Ap
C 41	64.4	1.5	3673778	13	US-10-312-841-2	Sequence 2, Appl1
42	64	1.5	5291	13	US-10-311-455-1292	Sequence 1292, Ap
43	64	1.5	5291	13	US-10-240-453-58	Sequence 58, Appl
44	64	1.5	8417	12	US-10-074-024-635	Sequence 635, App
C 45	63.8	1.4	744802	12	US-10-292-798-1369	Sequence 1369, Ap

ALIGNMENTS

RESULT 1

US-09-922-217-343/c
; Sequence 343, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922.217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-343

Query Match 12.5%; Score 552.2; DB 9; Length 646;
Best Local Similarity 93.0%; Pred. No. 2.6e-110;
Matches 609; Conservative 4; Mismatches 32; Indels 10; Gaps 3;
Qy 3419 AAAGCTTTCAGCCCTTCCTAGGACAGAGAAATGGGTAGCCCAATCTGCAATTTCTACT 3478
Db 645 AAAGCTTTCAGCCCTTCCTAGGACAGAGAAATGGGTAGCCCAATCTGCAATTTCTACT 586

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QY 3479 ACAGGCAATTGAGACCAAGTATGAAATTTATGAGAGTATGAAACATTTAAATT 3538
DB |||||||
DB 585 ACAGGCAATTGAGACCAAGTATGAAATTTATGAGAGTATGAAACATTTAAATT 526
QY 3539 ATGATAGTGTATGACATTTGATAGACATGCGATCTTTAGAGTATGAGAGTATGACAGGC 3598
DB |||||||
DB 525 ATGATAGTGTATGACATTTGATAGACATGCGATCTTTAGAGTATGAGAGTATGACAGGC 466
QY 3599 ATATTAGTGTATGAAATGAGTCAATTTGAGTCTTTAATAGCCATGATCAATAATTACCA 3658
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DB 465 ATATTAGTGTATGAAATGAGTCAATTTGAGTCTTTAATAGCCATGATCAATAATTACCA 406
QY 3659 AGTGAAGCTGTGGAACATATGCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 3718
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DB 405 AGTGAAGCTGTGGAACATATGCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 346
QY 3719 AATATTGTTCTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3778
DB |||||||
DB 345 AATATTGTTCTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 286
QY 3779 TTTTATATTGTTCAATTTATGAATATAATGAATGAGGAGTTCTGGTACCTCCTGTCTTT 3838
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DB 285 TTTTATATTGTTCAATTTATGAATATAATGAATGAGGAGTTCTGGTACCTCCTGTCTTT 227
QY 3839 ACAATATTGTTCCATTTGCGTCTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 3898
DB |||||||
DB 226 ACAATATTGTTCCATTTGCGTCTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 171
QY 3899 AGGTGGATGTTTCCATTTGCGTCTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 3958
DB |||||||
DB 170 TGAATG-----TTTCAATTTTGGTTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 116
QY 3959 AGAATTTCTTTATACATTTAGTCAAGTCTCTTGYCGGATATACGTTATGAGATATTA 4018
DB |||||||
DB 115 AGAATTTCTTTATACATTTAGTCAAGTCTCTTGYCGGATATATGTTATGAGATATTA 56
QY 4019 CACCTAGTCTGTGGCTTGAATTTCTTTATGCTTTTATGCTTTTATGATGAAGTATTT 4073
DB |||||||
DB 55 CACCTAGTCTGTGGCTTGAATTTCTTTATGCTTTTATGCTTTTATGATGAAGTATTT 1

RESULT 2
US-09-833-263-343/c
; Sequence 343, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-343

Query Match 12.5%; Score 552.2; DB 10; Length 646;
Best Local Similarity 93.0%; Pred. No. 2.6e-110;
Matches 609; Conservative 4; Mismatches 32; Indels 10; Gaps 3;

QY 3419 AAAAGCTTCTCAGCCTTCCAGGACAGAAATTTGGGTAGGCGCAATCTGCAATTTCTACT 3478
DB |||||||
DB 645 AAAAGCTTCTCAGCCTTCCAGGACAGAAATTTGGGTAGGCGCAATCTGCAATTTCTACT 586
QY 3479 ACAGGCAATTGAGACCAAGTATGAAATTTATGAGAGTATGAAACATTTAAATT 3538
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DB 585 ACAGGCAATTGAGACCAAGTATGAAATTTATGAGAGTATGAAACATTTAAATT 526
QY 3539 ATGATAGTGTATGACATTTGATAGACATGCGATCTTTAGAGTATGAGAGTATGACAGGC 3598
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DB 525 ATGATAGTGTATGACATTTGATAGACATGCGATCTTTAGAGTATGAGAGTATGACAGGC 466
QY 3599 ATATTAGTGTATGAAATGAGTCAATTTGAGTCTTTAATAGCCATGATCAATAATTACCA 3658
DB |||||||
DB 465 ATATTAGTGTATGAAATGAGTCAATTTGAGTCTTTAATAGCCATGATCAATAATTACCA 406
QY 3659 AGTGAAGCTGTGGAACATATGCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 3718
DB |||||||
DB 405 AGTGAAGCTGTGGAACATATGCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 346
QY 3719 AATATTGTTCTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3778
DB |||||||
DB 345 AATATTGTTCTGTGTCATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 286
QY 3779 TTTTATATTGTTCAATTTATGAATATAATGAATGAGGAGTTCTGGTACCTCCTGTCTTT 3838
DB |||||||
DB 285 TTTTATATTGTTCAATTTATGAATATAATGAATGAGGAGTTCTGGTACCTCCTGTCTTT 227
QY 3839 ACAATATTGTTCCATTTGCGTCTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 3898
DB |||||||
DB 226 ACAATATTGTTCCATTTGCGTCTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 171
QY 3899 AGGTGGATGTTTCCATTTGCGTCTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 3958
DB |||||||
DB 170 TGAATG-----TTTCAATTTTGGTTTAAATTTGATATCCCTGATAGCTATATTCGGTGCAT 116
QY 3959 AGAATTTCTTTATACATTTAGTCAAGTCTCTTGYCGGATATACGTTATGAGATATTA 4018
DB |||||||
DB 115 AGAATTTCTTTATACATTTAGTCAAGTCTCTTGYCGGATATATGTTATGAGATATTA 56
QY 4019 CACCTAGTCTGTGGCTTGAATTTCTTTATGCTTTTATGCTTTTATGATGAAGTATTT 4073
DB |||||||
DB 55 CACCTAGTCTGTGGCTTGAATTTCTTTATGCTTTTATGCTTTTATGATGAAGTATTT 1
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RESULT 3
US-10-025-380-343/c
; Sequence 343, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-380-343
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Db 61 AGAAGTGAAGAAATGGAACAGTGAAGAAATGAGGCAATATTTCCATGATCTCCCTGTAA 120
QY 3250 ACAGAAAGCAACAGAAAGGCAAGAGGCTGGCTCTACATCACTCTACCTTCCAAATCTT 3309
Db 121 ACAGAAAGCAACAGAAAGGCAAGAGGCTGGCTCTACATCACTCTACCTTCCAAATCTT 180
QY 3310 GTGAAGTGCATCTACTTCCAGAACCAAAATTAACCTTCAAGTCTCGCTGCTTGC 3369
Db 181 GTGAAGTGCATCTACTTCCAGAACCAAAATTAACCTTCAAGTCTCGCTGCTTGC 240
QY 3370 AGGTGGAATCCAGTCTGCAAGGAGTTAGGAAATGAAGGCTCTTTTAAAGCTTCTC 3429
Db 241 AGGTGGAATCCAGTCTGCAAGGAGTTAGGAAATGAAGGCTCTTTTAAAGCTTCTC 300
QY 3430 AGCTTCTCCTAGGACAGAAATGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 3489
Db 301 AGCTTCTCCTAGGACAGAAATGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 360
QY 3490 GACCAAGTTAGATTTGAAATATTAAGAGGTTATGAACCTTAAATTAATGATAGTGT 3549
Db 361 GACCAAGTTAGATTTGAAATATTAAGAGGTTATGAACCTTAAATTAATGATAGTGT 420
QY 3550 ATGACATTTGATGAACATGGGATCTTTAGAAAGTGAATTTGACAGGCATATTTAGTTGA 3609
Db 421 ATGACATTTGATGAACATGGGATCTTTAGAAAGTGAATTTGACAGGCATATTTAGTTGA 480
QY 3610 TGAATGGAGTCATTTGAGTCTTTTAAATAGCCATGTATCATAATTTACCAAGTGAAGCTGG 3669
Db 481 TGAATGGAGTCATTTGAGTCTTTTAAATAGCCATGTATCATAATTTACCAAGTGAAGCTGG 540
QY 3670 T 3670
Db 541 T 541

RESULT 6

US-10-146-502-1737
; Sequence 1737, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146.502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1737
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-1737

Query Match 12.2%; Score 537.4; DB 15; Length 541;
Best Local Similarity 99.4%; Pred. No. 4e-107;
Matches 538; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3130 ACCGTGTATCCAGCAAGAGGAGTCCAGTCAAGAGTCACTACAACTGATTTT 3189
Db 1 ATCTGTATCCAGCAAGAGGAGTCCAGTCAAGAGTCACTACAACTGATTTT 60
QY 3190 AGAAGTGAAGAAATGGAACAGTGAAGAAATGAGGCAATATTTCCATGATCTCCCTGTAA 3249
Db 61 AGAAGTGAAGAAATGGAACAGTGAAGAAATGAGGCAATATTTCCATGATCTCCCTGTAA 120
QY 3250 ACAGAAAGCAACAGAAAGGCAAGAGGCTGGCTCTACATCACTCTACCTTCCAAATCTT 3309

Db 121 ACAGAAAGCAACAGAAAGGCAAGAGGCTGGCTCTACATCACTCTACCTTCCAAATCTT 180
QY 3310 GTGAAGTGCATCTACTTCCAGAACCAAAATTAACCTTCAAGTCTCGCTGCTTGC 3369
Db 181 GTGAAGTGCATCTACTTCCAGAACCAAAATTAACCTTCAAGTCTCGCTGCTTGC 240
QY 3370 AGGTGGAATCCAGTCTGCAAGGAGTTAGGAAATGAAGGCTCTTTTAAAGCTTCTC 3429
Db 241 AGGTGGAATCCAGTCTGCAAGGAGTTAGGAAATGAAGGCTCTTTTAAAGCTTCTC 300
QY 3430 AGCTTCTCCTAGGAAACAGAAATTTGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 3489
Db 301 AGCTTCTCCTAGGAAACAGCAATTTGGGTGAGCAATCTGCAATTTCTACTACAGGCATTTGA 360
QY 3490 GACCAAGTTAGATTTGAAATATTAAGAGGTTATGAACCTTAAATTAATGATAGTGT 3549
Db 361 GACCAAGTTAGATTTGAAATATTAAGAGGTTATGAACCTTAAATTAATGATAGTGT 420
QY 3550 ATGACATTTGATGAACATGGGATCTTTAGAAAGTGAATTTGACAGGCATATTTAGTTGA 3609
Db 421 ATGACATTTGATGAACATGGGATCTTTAGAAAGTGAATTTGACAGGCATATTTAGTTGA 480
QY 3610 TGAATGGAGTCATTTGAGTCTTTTAAATAGCCATGTATCATAATTTACCAAGTGAAGCTGG 3669
Db 481 TGAATGGAGTCATTTGAGTCTTTTAAATAGCCATGTATCATAATTTACCAAGTGAAGCTGG 540
QY 3670 T 3670
Db 541 T 541

RESULT 7

US-10-102-524-532
; Sequence 532, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102.524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 532
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-532

Query Match 11.5%; Score 507; DB 15; Length 587;
Best Local Similarity 93.6%; Pred. No. 1.8e-100;
Matches 559; Conservative 4; Mismatches 24; Indels 10; Gaps 3;
QY 3419 AAAAGCTTCTCAGCCTTCTTAGGGAACAGAAATTTGGGTGAGCCAAATCTGCAATTTCTACT 3478
Db 1 AAAAGCTTCTCAGCCTTCTTAGGGAACAGAAATTTGGGTGAGCCAAATCTGCAATTTCTACT 60
QY 3479 ACAGGCATTTGAGACCAAGTATGATTTGAAATATTAATAGAGGTTATGAACCTTAAAT 3538
Db 61 ACAGGCATTTGAGACCAAGTATGATTTGAAATATTAATAGAGGTTATGAACCTTAAAT 120
QY 3539 ATGATAGTGGTATGACATTTGGATAGAACATGGGATCTTTTAGAAGTAGAATTCACAGGC 3598
Db 121 ATGATAGTGGTATGACATTTGGATAGAACATGGGATCTTTTAGAAGTAGAATTCACAGGC 180
QY 3599 ATATTAGTGTGAAATGAGTCAATTTGAGTCTTTTAAATAGCCATGTATCATAATTTACCA 3658

Db 181 ATATTAGTGTGAATGGAGTCATTTGAGTCTCTTAATAGCCATGTATCAATATTACCA 240
Qy 3659 AGTGAAGCTGGTGAACATATGCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 3718
Db 241 AGTGAAGCTGGTGAACATATGCTCCATTTTACAGTTAAGGAATATAATGGACAGATT 300
Qy 3719 AATATTGTTCTGTGATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 3778
Db 301 AATATTGTTCTGTGATGCCCAATCCCTTTCTAAGGAAGACTGCCCTACTATAGCAG 360
Qy 3779 TTTTATATTGTCATTTATGAATATAATGAATGAGGAGTTCTGTGACCTCCCTGTCTTT 3838
Db 361 TTTTATATTGTCATTTATGAATATAATGAATGA- GAGTTCTGGTACCTCCCTGTCTTT 419
Qy 3839 ACAAATATGGGTGTTGTCAGTATTTTCCCTTTTAAACMTTCCCAATTCGGGTGTGT 3898
Db 420 ACAAATATGG- - - - - TGTGTGACGATTTTTCCTTTTAAACCATTCCTGCTGTAG 475
Qy 3899 AGGTGGATGTTCCATTTGGGTTTTTAATTTGTATATCCCTGATAGCTATTAATGGGTGAT 3958
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Qy 3959 AGAAATCTTTATACATCTAGATGCAAGTCTCTTGGCGGATATACGTATTGAGATA 4015
Db 531 AGAAATCTTTATACATCTAGATGCAAGTCTCTTGGCGGATATATGATTTGAGATA 587

RESULT 8
US-09-918-995-13834
; Sequence 13834, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13834
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(468)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-13834

Query Match 9.2%; Score 405.6; DB 11; Length 468;
Best Local Similarity 97.4%; Pred. No. 2.3e-78;
Matches 411; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
Qy 2938 TGGTCTTACTAGCTGGGTGGTCTGTGTTGAGCTTATTTAGAGTCTAGTTTTCCTA 2997
Db 47 TCGTCTTACTAGCTGGGTGGTCTGTGTTGAGCTTATTTAGAGTCTAGTTTTCCTA 106
Qy 2998 CTTATAAGTAGAATGGTGGATTTGTTTCTTTTCTACCTAAAGGGAGATGGTAAGA 3057
Db 107 CTTATAAGCAGAAACGGGAGATTGTTTGTCTTCTACCTAAAGGGAGATGGCAAGA 166
Qy 3058 AACATGAATGCTTTTTTCAACTTTATTTGACAAAGTATTTCAAGTCTGTGTTCAAAA 3117
Db 167 AACAAATGAATGCTTTTTTCAAACTTTATTTGACGAGTGAITTTTCACTGTGTGTTCAAAA 226
Qy 3118 ATATATTGATGCTGCTGTATCCAGCAAGAGGAGTTCCAGTCAAGAGTCACTTACAACT 3177
Db 227 ATATATTGATGCTGCTGTATCCAGCAAGAGGAGTTCCAGTCAAGAGTCACTTACAACT 286
Qy 3178 GATTAGTGTGTTAGGAATGGAATGGAACAGTGGAGGAATGGAGGCCATATTTCATGA 3237

Db 287 GATTAGTGTGTTAAAGAAATGGAACAGTGGAGGAATGGAGGCCATATTTCATGA 346
Qy 3238 CTTCCCTTTTAAACAGAACAGAGGACAGAGGCTGGCTCTTACATCACTCTCAC 3297
Db 347 CTTCCCTTTTAAACAGAACAGAGGACAGAGGCTGGCTCTTACATCACTCTCAC 406
Qy 3298 CTTCCAAATCTTGGGAAGTGCATCTACTTTGCCAGAACCAAAATTAATTTCTTCCAAAGTT 3357
Db 407 CTTCCAAATCTTGGGAAGTGCATCTACTTTGCCAGAACCAAAATTAATTTCTTCCAAAGTT 466
Qy 3358 CT 3359
Db 467 CT 468

RESULT 9
US-09-783-590-3449
; Sequence 3449, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16, 2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3449
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (115)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (327)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (328)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (329)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (359)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3449

BEST AVAILABLE COPY

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Qy	3421	AAGCTTCTCAGCCCTCCTAGGG		3442	
Db	308	AAGCTTCTCAGNCTTTCTAGG		329	

RESULT 14

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US-09-960-352-8727
; Sequence 8727, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wyatt, John C.
; APPLICANT: Mathalaquan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8727
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 37-LIB34-077-Q1-E1-B10
US-09-960-352-8727

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Query Match	3.8%;	Score 167.6;	DB 10;	Length 315;
Best Local Similarity	76.3%;	Pred. No. 1.9e-26;		
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	QY		
1017	ACTGTGATCCTCAGGGCCATCCCACTACAGGATTAAGACAACTCCAGGACCAAGCC	1076	
	Db		
135	ACTGTGATCATACGGCGAGCCAGTACAGGATTGAAGACAACTCCAGGTCCTCAACC	194	
	QY		
1077	TTTCACAAGCGTGTGAGTTGATGAAAAAATAATGCCAAGCGCCCACTGTAACACTACAA	1136	
	Db		
195	TTTCCCAAGCCTTAAACCCCAATGAGAGTTTATGCCAATGCTCAGTGAATACGACAA	254	
	QY		
1137	CATACGTAGCTGACAGAAATCAGACAAG	1166	
	Db		
255	CATATGTAGCTGACAGAAATCAGACAATG	284	

RESULT 15

US-09-864-761-11287
 ; Sequence 11287, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aecmica-x-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04

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, PRIOR APPLICATION NUMBER: US 60/207,456
, PRIOR FILING DATE: 2000-05-26
, PRIOR APPLICATION NUMBER: US 09/632,366
, PRIOR FILING DATE: 2000-08-03
, PRIOR APPLICATION NUMBER: GB 24263.6
, PRIOR FILING DATE: 2000-10-04
, PRIOR APPLICATION NUMBER: US 60/236,359
, PRIOR FILING DATE: 2000-09-27
, PRIOR APPLICATION NUMBER: PCT/US01/006666
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006657
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006664
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006669
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006665
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006668
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006663
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006662
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006661
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: PCT/US01/006670
, PRIOR FILING DATE: 2001-01-30
, PRIOR APPLICATION NUMBER: US 60/234,687
, PRIOR FILING DATE: 2000-09-21
, PRIOR APPLICATION NUMBER: US 09/608,408
, PRIOR FILING DATE: 2000-06-30
, PRIOR APPLICATION NUMBER: US 09/774,203
, PRIOR FILING DATE: 2001-01-29
, NUMBER OF SEQ ID NOS: 49117
, SOFTWARE: Annonax Sequence Listing Engine
, SEQ ID NO 11287
, LENGTH: 442
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: MAP TO AB013139.1
, OTHER INFORMATION: EXPRESSED IN BRAIN, S
, OTHER INFORMATION: EXPRESSED IN BONE MAR
, OTHER INFORMATION: EXPRESSED IN PLACENTA
, OTHER INFORMATION: EXPRESSED IN LUNG, S
, OTHER INFORMATION: EXPRESSED IN ADULT L
US-09-864-761-11287

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Query Match 2.7%; Score 119.4; DB 9; Length 442;
Best Local Similarity 99.2%; Pred. No. 7.9e-16;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	2238	T 2238	
Db	384	T 384	

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